167257

From:	Yu, Misook
Sent:	Thursday, September 29, 2005 9:19 AM
To:	STIC-Biotech/ChemLib
Subject:	09/670,568

Pls do Interference search only for SEQ ID NO:2, and DNA encoding SEQ ID NO:1

Examiner Misook Yu, Ph.D.
571-272-0839 (Phone)
Art Unit 1642
REM-3A18 (Room)
REM-3C18 (Mail Box)

****
Searcher:_____
Searcher Phone:_____ 22504
Date Searcher Picked up: 10 13 05
Date completed:___ 10 3 05
Searcher Prep Time:_____ 6
Online Time:_____ 10

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:____✓____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:__✓__
WWW/Internet:_____
Other (Specify):_____

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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    October  3, 2005, 06:02:33  ; Search time 454 Seconds
                                        (without alignments)
                                        10149.241 Million cell updates/sec

Title:          US-09-670-568C-2
Perfect score:  2816
Sequence:       1 tcgttgatatcaaagacagt..........gcatcctggtttaaaagaaa 2816
Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched:       1202784 seqs, 818118359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES
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Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2816	100.0	2816	3	US-09-643-597-333	Sequence 333, App
2	2816	100.0	2816	4	US-09-542-615A-333	Sequence 333, App
3	2816	100.0	2816	4	US-09-606-421B-333	Sequence 333, App
4	2816	100.0	2816	4	US-09-630-940B-333	Sequence 333, App
5	2798	99.4	2810	4	US-09-949-016-5447	Sequence 5447, Ap
6	1433	50.9	255679	4	US-09-949-016-17189	Sequence 17189, A
7	1376	48.9	2270	3	US-09-643-597-332	Sequence 332, App
8	1376	48.9	2270	4	US-09-542-615A-332	Sequence 332, App
9	1376	48.9	2270	4	US-09-606-421B-332	Sequence 332, App
10	1376	48.9	2270	4	US-09-630-940B-332	Sequence 332, App
11	1364	48.4	4849	3	US-09-643-597-335	Sequence 335, App
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13	1364	48.4	4849	4	US-09-606-421B-335	Sequence 335, App
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16	1232	43.8	1551	4	US-09-542-615A-337	Sequence 337, App
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19	1031.2	36.6	2082	3	US-09-643-597-334	Sequence 334, App
20	1031.2	36.6	2082	4	US-09-277-196-1	Sequence 1, Appli
21	1031.2	36.6	2082	4	US-09-542-615A-334	Sequence 334, App
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24	1028.6	36.5	1386	3	US-09-643-597-336	Sequence 336, App
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38	1026.4	36.4	2820	4	US-09-542-615A-331	Sequence 331, App
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43	244.2	8.7	1215	1	US-08-347-792-20	Sequence 20, Appl
44	244.2	8.7	1215	3	US-08-431-357-20	Sequence 20, Appl
45	244.2	8.7	1215	3	US-08-392-542-26	Sequence 26, Appl

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                                ALIGNMENTS

RESULT 1
US-09-643-597-333
; Sequence 333, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT: Fan, Liqun
;  APPLICANT: Kalos, Michael D.
;  APPLICANT: Bangur, Chaitanya S.
;  APPLICANT: Hosken, Nancy
;  APPLICANT: Fanger, Gary R.
;  APPLICANT: Li, Samuel X.
;  APPLICANT: Wang, Aijun
;  APPLICANT: Skeiky, Yasir A.W.
;  APPLICANT: Henderson, Robert A.
;  APPLICANT: McNeill, Patricia D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C11
;  CURRENT APPLICATION NUMBER: US/09/643,597
;  CURRENT FILING DATE: 2000-08-21
;  NUMBER OF SEQ ID NOS: 369
;  SOFTWARE: FastSEQ for Windows Version 3.0
;
;  SEQ ID NO 333
;  LENGTH: 2816
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-643-597-333

  Query Match             100.0%;  Score 2816;  DB 3;  Length 2816;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2816;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy        121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180
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Qy        181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240
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Qy        241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGAATTGAGATT 300
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[handwritten note: prot 347]

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Qy  1561 TGTGTGTGCGTGTGTATCAGCCCTCATAAACAGGACTTGAGCACTTGGCTCAGAGA 1620
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Qy  2161 GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTATGTCTAAAGTTTTTCTTGTA 2220
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Qy  2221 CATGAAACCCTGGAAGACCTACTACAAAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280
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Qy   481  CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCCTCCAACACCGACTAC  540
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Db   661  CAGATCAAGGTGATGACCCCACCTCCTCCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720

Qy   721  AAAAAAGTGAGCACGTCACGGAGGTGGTGAAGGGTGCCCAACCATGAGCTGAGCCGT  780
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GAATTCAACGAGGGACAGATTGCCCTCCTAGTCATTTGATTCGAGTGAGGGAACAGC  840

Qy   841  CATGCCCAGTATGTAGAAGATCCATCACAGGAGGAGCAGAGTGTGCTGGTACCTTATGAG  900
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Qy   961  TGTGTTGGAGGATGAACCGCCGACGCTGCTTGTGTTGCCCGGAAGAGAT  1020
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Qy   1021 GGGCAAGTCCTGGGCCGACGCTGCTTTGAGGCCCGGATCTGTGTTGCCCAGGAAGAGAC  1080
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Db   1021 GGGCAAGTCCTGGGCCGACGCTGCTTTGAGGCCCGGATCTGTGTTGCCCAGGAAGAGAC  1080

Qy   1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT  1140

Qy   1141 GATGGTACGAAGGCGCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGGTACGAAGGCGCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG  1200

Qy   1201 AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGGCGTGAGACTTAT  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGGCGTGAGACTTAT  1260

Qy   1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA  1320

Qy   1321 ATTGAAACTACAGGCAACAGCAGCAGCACCACTTACTTCAGAAACATCTC  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGAAACTACAGGCAACAGCAGCAGCACCACTTACTTCAGAAACATCTC  1380
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Qy   2461 CTGATACTGTTCAGTGAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTGATACTGTTCAGTGAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC  2520

Qy   2521 AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTAAAGGGTAGAGACTACTT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTAAAGGGTAGAGACTACTT  2580

Qy   2581 TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTCTTCCATTTTAAAAACATATT  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTCTTCCATTTTAAAAACATATT  2640

Qy   2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCTCCATCCTTCCCACACCCAGT  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCTCCATCCTTCCCACACCCAGT  2700

Qy   2701 CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT  2760

Qy   2761 TTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTGGTTTAAAGAAA  2816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTGGTTTAAAGAAA  2816
```

RESULT 2
US-09-542-615A-333

; Sequence 333, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-333

Query Match   100.0%;   Score 2816;   DB 4;   Length 2816;
Best Local Similarity 100.0%;   Pred. No. 0;   Indels   0;   Gaps   0;
Matches 2816;   Conservative 0;   Mismatches 0;   Pred No. 0;

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Qy   1    TCCTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGTGTGTGCCACCCT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1    TCCTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGTGTGTGCCACCCT  60

Qy   61   ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120

Qy   121  AAAGAAAGTTATTACCGGATCCACCATCCACGTCCCAGAGCACACACAGCAAATGAATTCCTCAGT  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AAAGAAAGTTATTACCGGATCCACCATCCACGTCCCAGAGCACACACAGCAAATGAATTCCTCAGT  180

Qy   181  CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAACAGCGTTTATATGTTCAGTTCAGCCC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAACAGCGTTTATATGTTCAGTTCAGCCC  240

Qy   241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGCATCAGAAGCAGCCGGCAAACAAGATTGAGATT  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGCATCAGAAGCAGCCGGCAAACAAGATTGAGATT  300
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RESULT 3
US-09-606-421B-333
; Sequence 333, Application US/09606421B
; Patent No. 6531315
GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-333

  Query Match   100.0%; Score 2816; DB 4; Length 2816;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 2816; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 TCGTTGATATCAAAGACAGTTGAAGGAATGAATTTTGAAACTTCACGGTGTGCCACCCTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCGTTGATATCAAAGACAGTTGAAGGAATGAATTTTGAAACTTCACGGTGTGCCACCCT 60

Qy   61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCAGCTCATTCTTCTTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCAGCTCATTCTTCTTGG 120

Qy   121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAATTCCTCAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAATTCCTCAGT 180

Qy   181 CCAGAGGTTTCCAGCATATCTGGATTTTCTGAACAGCCTATATGTTCAGTCAGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGAGGTTTCCAGCATATCTGGATTTTCTGAACAGCCTATATGTTCAGTCAGCCC 240

Qy   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGTGGCAAAACAAGATGAGATT 300

Qy   1381 CTTTCAGCCGCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAAACTCCAAAACAATCT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTTCAGCCGCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAAACTCCAAAACAATCT 1440

Qy   1441 GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC 1500

Qy   1501 TCTATATTTAAGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTGTA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCTATATTTAAGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTGTA 1560

Qy   1561 TGTGTGTGCGTGTGTATCGTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGTGTGTGCGTGTGTATCGTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA 1620

Qy   1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACCT 1680

Qy   1681 TTACAAGAAAGGATGTGTTTTCTGCAGATTTGTATCCTAGACCGGCCATTGGTGGGTGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TTACAAGAAAGGATGTGTTTTCTGCAGATTTGTATCCTAGACCGGCCATTGGTGGGTGAG 1740

Qy   1741 GAACCACTGTGTTTGTTTGTCTGTGAGCTTTCTGTGTTTCCTGGGAGGGGAGGGGTCAGGTGGG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GAACCACTGTGTTTGTTTGTCTGTGAGCTTTCTGTGTTTCCTGGGAGGGGAGGGGTCAGGTGGG 1800

Qy   1801 GAAAGGGGCATTAAGATGTTATTGGAACCCTTTCTGTCCTTCTGTCTTCTGTGTTTTTCTAA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAAAGGGGCATTAAGATGTTATTGGAACCCTTTCTGTCCTTCTGTCTTCTGTGTTTTTCTAA 1860

Qy   1861 AATTCACAGGAAGCTTTGAGCAGGTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AATTCACAGGAAGCTTTGAGCAGGTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920

Qy   1921 AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTGTAGGTGACTGAGACTCAGTCAGA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTGTAGGTGACTGAGACTCAGTCAGA 1980

Qy   1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGAAACGGAGGTGTCAAGTG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGAAACGGAGGTGTCAAGTG 2040

Qy   2041 TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGGAGAGTTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGGAGAGTTC 2100

Qy   2101 TTTGTGAGAACTTGCATTATTTGTGTCCCCTCATGTGTAGGTAGGTAGAACATTTCTTAAT 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTTGTGAGAACTTGCATTATTTGTGTCCCCTCATGTGTAGGTAGGTAGAACATTTCTTAAT 2160

Qy   2161 GCTGTGTACCTGCCCTCTGCCACTGTACCTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCCTTGTA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCTGTGTACCTGCCCTCTGCCACTGTACCTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCCTTGTA 2220

Qy   2221 CATGAACCCTGAAGACCTACTACACAAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATGAACCCTGAAGACCTACTACACAAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280

Qy   2281 CTCATTTTGTGCTTTAATGAAGAGACAAATCCACCCCAGTAATATTGCCCTTTACGTAGT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CTCATTTTGTGCTTTAATGAAGAGACAAATCCACCCCAGTAATATTGCCCTTTACGTAGT 2340

Qy   2341 TGTTTACCATTATTCAAAGCTTCCATCCCTCCACCTACCTAAAAACCAGCCATATTA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGTTTACCATTATTCAAAGCTTCCATCCCTCCACCTACCTAAAAACCAGCCATATTA 2400

Qy   2401 AATTTGCTTAATTAGAGCTTCCATCCCTCCAGCCTTCCAGCCTCCACCTACCTAAAAACCAGCCATATTA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AATTTGCTTAATTAGAGCTTCCATCCCTCCAGCCTTCCAGCCTCCACCTACCTAAAAACCAGCCATATTA 2460

Qy   2461 CTGATACTGTTCAGTGCATTGCATTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTGATACTGTTCAGTGCATTGCATTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCAGCTACTT 2520

Qy   2521 AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy   2581 TTCTTTTTTTTACTCAAAGTTTAGAGAATCTCTGTTCTTCTTTCCATTTTAAAAACATATT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTCTTTTTTTTACTCAAAGTTTAGAGAATCTCTGTTCTTCTTTCCATTTTAAAAACATATT 2640

Qy   2641 TTAAGATAATAGCATAAAGACTTAAAAATGTTAAAAATGTTCCTCCCCTCCATCTTCCCACACCCAGT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TTAAGATAATAGCATAAAGACTTAAAAATGTTAAAAATGTTCCTCCCCTCCATCTTCCCACACCCAGT 2700

Qy   2701 CACCAGCACTGTATTTTCTGTCACCAGACAATGATTTCTGTTATTGGGCTGTTGCTT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CACCAGCACTGTATTTTCTGTCACCAGACAATGATTTCTGTTATTGGGCTGTTGTGCTT 2760

Qy   2761 TTGTGGATGTGTGATTTAATTTTCAATAAACTTTGCAT TTGGTTTAAAAGAAA 2816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTGTGGATCGTGTGATTTAATTTTCAATAAACTTTGCAT TTCGGTTTAAAAGAAA 2816

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Db   241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGTGCGACAAACAAGATTGAGATT  300

Qy   301  AGCATGGACTGTATCCGCATGCAGGACTCGGAGTGCCACCATGTGGCCACCAGTAC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGCATGGACTGTATCCGCATGCAGGACTCGGAGTGCCACCATGTGGCCACCAGTAC  360

Qy   361  ACGAACCTGGGGCTCCTGAACACAGCAGCAGATTCAGAACGGCTCCTCGTCCACC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACGAACCTGGGGCTCCTGAACACAGCAGCAGATTCAGAACGGCTCCTCGTCCACC  420

Qy   421  AGTCCCTATAACACAGACCACGCGCAGAACAGCGCGCCCTCGCCCTACGCACAG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AGTCCCTATAACACAGACCACGCGCAGAACAGCGCGCCCTCGCCCTACGCACAG  480

Qy   481  CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCCTCCAACACCGACTAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CCCAGCTCCACCTTCGATGCTCTCTCCATCACCGCCATCCCCTCCAACACCGACTAC  540

Qy   541  CCAGGCCCGCACAGTTCGCACGTGTCCTTCAGCAGTCGACGCACCGCCAAGTCGGCCACC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CCAGGCCCGCACAGTTCGCACGTGTCCTTCAGCAGTCGACGCACCGCCAAGTCGGCCACC  600

Qy   601  TGGACGTATTCCACTGAACTCTACTGCCAAATTGAAAGACATGCCCCATC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGGACGTATTCCACTGAACTCTACTGCCAAATTGAAAGACATGCCCCATC  660

Qy   661  CAGATCAAGGTGATGAGCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720
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Db   661  CAGATCAAGGTGATGAGCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720

Qy   721  AAAAAAGCTGAGCACGTCACGGAGGTGTGAAGCGGTGCCCAACCATGAGTCGAGCGT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AAAAAAGCTGAGCACGTCACGGAGGTGTGAAGCGGTGCCCAACCATGAGTCGAGCGT  780

Qy   781  GAATTCAACGAGGGACAGATTGCCCCTCCAGTCATTTGATTCGAGTAGAGGGAACAGC  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GAATTCAACGAGGGACAGATTGCCCCTCCAGTCATTTGATTCGAGTAGAGGGAACAGC  840

Qy   841  CATGCCCAGTATGTGAAGATCCCATCACAGGAGACACAGAGTGTGCTGTGTACCCTTATGAG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CATGCCCAGTATGTGAAGATCCCATCACAGGAGACACAGAGTGTGCTGTGTACCCTTATGAG  900

Qy   901  CCACCCCAGGTTGGCACTGAATTCAGCGACGCTGCTTCACGAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CCACCCCAGGTTGGCACTGAATTCAGCGACGCTGCTTCACGAGTCTTGTACAATTTCATGTGTAACAGCAGT  960

Qy   961  TGTGTTGGAGGATGAACCGCCCGTCCAATTTTACTGTTACTCTGAAACCAGAGAT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TGTGTTGGAGGATGAACCGCCCGTCCAATTTTACTGTTACTCTGAAACCAGAGAT  1020

Qy  1021  GGGCAAGTCCTGGGCGACGCTGCTTTGAGGCCCGATCGTGCTTGCTTGGACAGTACAAAGCATCCATCAAG  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGGCAAGTCCTGGGCGACGCTGCTTTGAGGCCCGATCGTGCTTGCTTGGACAGTACAAAGCATCCATCAAG  1080

Qy  1081  AGGAAGGGCGATGGAAGGCCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGCAGTTCGGACAGTACAAGAACGT  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  AGGAAGGGCGATGGAAGGCCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGCAGTTCGGACAGTACAAGAACGT  1140

Qy  1141  GATGGTACGAAGCGCCCGTTTCGTCAGAACACACACAGTGTATACCTTACCAGTGAGGGGCCGTGAGACTTAT  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GATGGTACGAAGCGCCCGTTTCGTCAGAACACACACAGTGTATACCTTACCAGTGAGGGGCCGTGAGACTTAT  1200

Qy  1201  AAACGAAGAGTCCCCAGATGAAGCAGCAGCAAGTTTCGGAACTTCCTCAGCACA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  AAACGAAGAGTCCCCAGATGAAGCAGCAGCAAGTTTCGGAACTTCCTCAGCACA  1260

Qy  1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAACTTCCTGGAACTTCCTGGAACTTCCTCAGCACACA  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAACTTCCTGGAACTTCCTCAGCACACA  1320

Qy  1321  ATTGAAACGTACAGGCAACAACAGCAGCAACAGCAGCAGCAGCACTTACTTCAGAAACATCTC  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ATTGAAACGTACAGGCAACAACAGCAGCAACAGCAGCAGCAGCACTTACTTCAGAAACATCTC  1380
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Qy  1381  CTTTCAGCGCTTGCTTCAGGAATGAGCTTGTGTGGAGCCCGGAGAGAAACTCCAAAACAATCT  1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CTTTCAGCGCTTGCTTCAGGAATGAGCTTGTGGGAGCCCGGAGAGAAACTCCAAAACAATCT  1440

Qy  1441  GACGGCTCTTCTTAGACATTCCAAGCCCAAACGATCAGTGTACCCATAGAGCCCTATC  1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GACGGCTCTTCTTAGACATTCCAAGCCCAAACGATCAGTGTACCCATAGAGCCCTATC  1500

Qy  1501  TCTATATTTTAAGTGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGTA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  TCTATATTTTAAGTGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGTA  1560

Qy  1561  TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620

Qy  1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT  1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT  1680

Qy  1681  TTACAAGAAGATGTTTTCTGCAGATTTGTATCCTTAGACGGCCATTGGTGGGTGAG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  TTACAAGAAGATGTTTTCTGCAGATTTGTATCCTTAGACGGCCATTGGTGGGTGAG  1740

Qy  1741  GAACCACTGTGTTTCTGTTGTTTCCTGGGGATGGGGAGGGGTCAGGTGGG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GAACCACTGTGTTTCTGTTGTTTCCTGGGGATGGGGAGGGGTCAGGTGGG  1800

Qy  1801  GAAAGGGCATTAGAATGTTTATTGGAACCCTTTCTGTCTCTTCTCTGTGTTTTTTCTAA  1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GAAAGGGGCATTAGAATGTTTATTGGAACCCTTTCTGTCTCTTCTCTGTGTTTTTCTAA  1860

Qy  1861  AATTCACAGGGAAGCTTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  AATTCACAGGGAAGCTTTTGAGCAGTCTCAAACTAAGATGTCTTTTAAGAAAAGGAG  1920

Qy  1921  AAAAAAGTTGTTATTTGTCTGTCGTGCATAAGTAAGTGTGATGACTCAGTCAGA  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  AAAAAAGTTGTTATTTGTCTGTCGTGCATAAGTAAGTGTGACTCAGTCAGTCAGA  1980

Qy  1981  CCCTTTAATGCTGTCATGTAATAATATTGCAAGTAGTAGTAGAAACGAAGGTGTCAAGTG  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CCCTTTAATGCTGTCATGTAATAATATTGCAAGTAGTAGTAGAAACGAAGGTGTCAAGTG  2040

Qy  2041  TACTGCTGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGAGTTC  2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TACTGCTGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGAGTTC  2100

Qy  2101  TTTGTGAGAACTTGCATTATTTGTCTCCCCTCATGTGTAGGTAGGAACATTCTTAAT  2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  TTTGTGAGAACTTGCATTATTTGTCTCCCCTCATGTGTAGGTAGGAACATTCTTAAT  2160

Qy  2161  GCTGTGTACCTGCCTCTGCCACTGTCGTATGTGTTGGCATCGTATGCTAAAGTTTTTCTTGTA  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCTGTGTACCTGCCTCTGCCACTGTCGTATGTGTTGGCATCGTATGCTAAAGTTTTTCTTGTA  2220

Qy  2221  CATGAAACCCTGAAGACTACTACAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CATGAAACCCTGAAGACTACTACAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2280

Qy  2281  CTCATTTTGTGCTTTTAATAGAACAAATCCACCCCCAGTAATATTGCCCTTACGTAGT  2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCCAGTAATATTGCCCTTACGTAGT  2340

Qy  2341  TGTTTACCATTATTCAAAGTCAAAATGGAATTTGAAGGCCCTCTCACAAAATCTGTGATT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  TGTTTACCATTATTCAAAGTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400

Qy  2401  AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAAACCAGCCATATTA  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAAACCAGCCATATTA  2460
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Qy  2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC  2520

Qy  2521  AGACGTGTTAAAATCAGCACTCCTGGACTGGGAATTAAAGATTGAAAGGGTAGACTACTT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  AGACGTGTTAAAATCAGCACTCCTGGACTGGGAATTAAAGATTGAAAGGGTAGACTACTT  2580

Qy  2581  TTCTTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTAAAAACATATT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  TTCTTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTAAAAACATATT  2640

Qy  2641  TTAAGATAATAGCATAAAGACTTAAAAATGTTCCTCCCCTCCATCTTCCCACACCCAGT  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TTAAGATAATAGCATAAAGACTTAAAAATGTTCCTCCCCTCCATCTTCCCACACCCAGT  2700

Qy  2701  CACCAGCACTGTATTTTCGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CACCAGCACTGTATTTTCGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT  2760

Qy  2761  TTGTGGATGTGTGATTTTAATTTCAATAAACTTTGCATCTTGGTTTAAAAGAAA  2816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTGTGGATGTGTGATTTTAATTTCAATAAACTTTGCATCTTGGTTTAAAAGAAA  2816
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RESULT 4
US-09-630-940B-333
; Sequence 333, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-333

Query Match   100.0%; Score 2816; DB 4; Length 2816;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT   300

Qy   301  AGCATGGACTGTATCCGCATGCCGGACTCGGACCTGAGTGGCCACCCATGTGGCCACAGTAC   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGCATGGACTGTATCCGCATGCCGGACTCGGACCTGAGTGGCCACCCATGTGGCCACAGTAC   360

Qy   361  ACGAACCTGGGGCTCCTGAACAGCATGGACAGCAGAGATTCAGGACGGCGCTCCTGTCCACC   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACGAACCTGGGGCTCCTGAACAGCATGGACAGCAGAGATTCAGGACGGCGCTCCTGTCCACC   420

Qy   421  AGTCCCTATAACACAGACCACCGGCAGAACACAGGCTCACGGCGCCCTCGCCCTACGCACAG   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AGTCCCTATAACACAGACCACCGGCAGAACACAGGCTCACGGCGCCCTCGCCCTACGCACAG   480

Qy   481  CCCAGCTCCACCTTCGATGCTCTCTCCATCCCCTCAACACCGACTAC   540
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CCCAGCTCCACCTTCGATGCTCTCTCCATCCCCTCAACACCGACTAC   540

Qy   541  CCAGGCCCGCACAGTTTCGACGTGTCCTTCCAGCAGTCGAGCACCGCCAGTCGGCCCACC   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CCAGGCCCGCACAGTTTCGACGTGTCCTTCCAGCAGTCGAGCACCGCCAGTCGGCCCACC   600

Qy   601  TGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACACATGCCCCATC   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACACATGCCCCATC   660

Qy   661  CAGATCAAGGTGATGACCGTGTTATCCGCGCCATGCCTTGTCTAC   720
          |||||||||||||||||||||||||||||||||||||||||||||
Db   661  CAGATCAAGGTGATGACCGTGTTATCCGCGCCATGCCTTGTCTAC   720

Qy   721  AAAAAGCTGAGCACGTCACGGAGGCGGTGCCCCAACCATGAGCTGAGCCGT   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AAAAAGCTGAGCACGTCACGGAGGCGGTGCCCCAACCATGAGCTGAGCCGT   780

Qy   781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCGAGTAGAGGGAACAGC   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCGAGTAGAGGGAACAGC   840

Qy   841  CATGCCCAGTATGTAGAGATCCCATCACAGAGAAGACAGAGTGTGCTGTGGACTTATGAG   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CATGCCCAGTATGTAGAGATCCCATCACAGAGAAGACAGAGTGTGCTGTGGACTTATGAG   900

Qy   901  CCACCCCAGGTTGGCACTGAATTCACGACAGCAGTCTTGTACAATTCATGTGTAACAGCAGT   960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CCACCCCAGGTTGGCACTGAATTCACGACAGCAGTCTTGTACAATTCATGTGTAACAGCAGT   960

Qy   961  TGTGTTGGAGGGATGAACCGCCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TGTGTTGGAGGGATGAACCGCCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT  1020

Qy  1021  GGGCCAAGTCCTCGGGCCGACGCTGCTTTGGAGGCCCGGATCCGGATTGCCCAGGAAGAGAC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGGCCAAGTCCTCGGGCCGACGCTGCTTTGGAGGCCCGGATCCGGATTGCCCAGGAAGAGAC  1080

Qy  1081  AGGAAGGCCGATGAAGATAGCATCAGAAGAGCAGCAGTTTCGGACAGTACAAAGAACCGGT  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  AGGAAGGCCGATGAAGATAGCATCAGAAGAGCAGCAGTTTCGGACAGTACAAAGAACCGGT  1140

Qy  1141  GATGGTACGAAGGCGCCCCGTTTCGTCAGAACACACAGGTATCCAGATGACATCATCAAG  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GATGGTACGAAGGCGCCCCGTTTCGTCAGAACACACAGGTATCCAGATGACATCATCAAG  1200

Qy  1201  AAACGAAGAATCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  AAACGAAGAATCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT  1260

Qy  1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAGCTATATGTTCAGTTCAGCCCACA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAGCTATATGTTCAGTTCAGCCCACA  1320
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Qy     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT   60

Qy    61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTTAGCGTTTCGTAGAAACCCAGCACACAGAATTCCTCTTGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTTAGCGTTTCGTAGAAACCCAGCACACAGAATTCCTCTTGG  120

Qy   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAATGAATTCCTCAGT  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAATGAATTCCTCAGT  180

Qy   181  CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
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RESULT 5
US-09-949-016-5447
; Sequence 5447, Application US/0994901G
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SEQ ID NO 5447
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   LENGTH: 2810
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5447

Query Match   99.4%; Score 2798; DB 4; Length 2810;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2809; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy  240 CATTGACTTGAACTTTGTGGATGAACCATCAGAGAGATGGTGGCACAAACAAGATTGAGAT 299
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CATTGACTTGAACTTTGTGGATGAACCATCAGAGAGATGGTGGCACAAACAAGATTGAGAT 300

Qy  300 TAGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTGACCTGGACTGGACCCACAGTA 359
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 TAGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTGACCTGGACTGGACCCACAGTA 360

Qy  360 CACGAACCTGGGGCTCCTGAACAGCAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCAC 419
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CACGAACCTGGGGCTCCTGAACAGCAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCAC 420

Qy  420 CAGTCCCTATAACACAGACACACGCGCAGAACAGCGTCACGCGGCCCCTGCCCTACGCACA 479
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 CAGTCCCTATAACACAGACACACGCGCAGAACAGCGTCACGCGGCCCCTGCCCTACGCACA 480

Qy  480 GCCCAGCTCCACCTTCGATGCTCTCTCCATCCCCGCCATCCCTTCCCACACCGACTA 539
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GCCCAGCTCCACCTTCGATGCTCTCTCCATCCCCGCCATCCCTTCCCACACCGACTA 540

Qy  540 CCCAGGCCCGCACAGTTCGACGTGTCCTTCAGCAGTCGAGCACCGCCAGTGCGGCCAC 599
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CCCAGGCCCGCACAGTTCGACGTGTCCTTCAGCAGTCGAGCACCGCCAGTGCGGCCAC 600

Qy  600 CTGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCAT 659
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 CTGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCAT 660

Qy  660 CCAGATCAAGGTGATGACCCCACCTCCTCAGGGAGTGTGTATCCGCGCCATGCCTGTCTA 719
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CCAGATCAAGGTGATGACCCCACCTCCTCAGGGAGTGTGTATCCGCGCCATGCCTGTCTA 720

Qy  720 CAAAAAAGCTGAGCGACACGTCACGGAGGTGGTGAAGCCGTGCCCAACCATGAGCTGAGCCG 779
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 CAAAAAAGCTGAGCGACACGTCACGGAGGTGGTGAAGCCGTGCCCAACCATGAGCTGAGCCG 780

Qy  780 TGAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGAATTGATTCAGTGAGTGGGGAACAG 839
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TGAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGAATTGATTCAGTGAGTGGGGAACAG 840

Qy  840 CCATGCCCAGTGATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGGTACCTTATGA 899
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 CCATGCCCAGTGATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGGTACCTTATGA 900

Qy  900 GCCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAG 959
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GCCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAG 960

Qy  960 TTGTGTTGGAGGGATGAACCGGCCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGA 1019
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TTGTGTTGGAGGGATGAACCGGCCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGA 1020

Qy 1020 TGGGCAAGTCCTGGGCACGCTGCTTTGAGGCCCGGATCTGGATCTGCTTGCCCAGGAAGAGA 1079
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGGGCAAGTCCTGGGCACGCTGCTTTGAGGCCCGGATCTGGATCTGCTTGCCCAGGAAGAGA 1080

Qy 1080 CAGGAAGGCGGATGAAGCGATGAACAGCATCAGAAAGAGCAAGTTTCGGACAGTACAAAGACACGG 1139
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CAGGAAGGCGGATGAAGCGATGAACAGCATCAGAAAGAGCAAGTTTCGGACAGTACAAAGACACGG 1140

Qy 1140 TGATGGTACGAAGCGCCCGTTTCGTCAGAACACACATGGTATCCGATGACATCCATCAA 1199
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TGATGGTACGAAGCGCCCGTTTCGTCAGAACACACATGGTATCCGATGACATCCATCAA 1200

Qy 1200 TGGGCAAGTCCTGGCCACGCTGCTTTGAGGGCCGTGAGACTTA 1259
        ||||||||||||||||||||||||||||||||||||||||||||
Db 1201 TGGGCAAGTCCTGGCCACGCTGCTTTGAGGGCCGTGAGACTTA 1260

Qy 1260 TGAAAATGCTGTTGAAGATCAAAGAGCAAGTTCCTGAACTCAGTGACACCTTCCTCAGCAGCAC 1319
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 TGAAAATGCTGTTGAAGATCAAAGAGCAAGTTCCTGAACTCAGTGACACCTTCCTCAGCAGCAC 1320

Qy 1320 AATTGAAACGTACAGGCAACAGCAACAACGCAGCAGCAGCACACTTACTTCAGAAACATCT 1379
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1380

Qy 1380 CCTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCGGGAGAAACTCCAAAACAATC 1439
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CCTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCGGGAGAAACTCCAAAACAATC 1440

Qy 1440 TGACGTCTTCTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTAT 1499
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 TGACGTCTTCTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTAT 1500

Qy 1500 CTCTATATTTTAAGTGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGT 1559
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 CTCTATATTTTAAGTGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGT 1560

Qy 1560 ATGTGTGTGCGTGTGTATCCAGCCCCATAAAACAGGACTTGAAGACACTTTGGCTCAGAG 1619
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 ATGTGTGTGCGTGTGTATCCAGCCCCATAAAACAGGACTTGAAGACACTTTGGCTCAGAG 1620

Qy 1620 ACCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACC 1679
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 ACCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACC 1680

Qy 1680 TTTACAGAAAGGATGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGA 1739
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 TTTACAGAAAGGATGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGA 1740

Qy 1740 GGAACCACTGTGTTGTCTGTGAGCTTTCGTTGTTGTTTCCTGGGAGGGAGGGGTCAGGTGG 1799
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 GGAACCACTGTGTTGTCTGTGAGCTTTCGTTGTTGTTTCCTGGGAGGGAGGGGTCAGGTGG 1800

Qy 1800 GGAAAGGGCATTAAGATGTTTATTGGAACCCTTTCTCGTCTTTCTGTCTTCTCTGTTTTCTA 1859
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 GGAAAGGGCATTAAGATGTTTATTGGAACCCTTTCTCGTCTTTCTGTCTTCTCTGTTTTCTA 1860

Qy 1860 AAATTCACAGGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGA 1919
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 AAATTCACAGGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGA 1920

Qy 1920 GAAAAAAGTTGTTATTGTCTGTGCATAAGTAAGTGTGTCATAAGTAAGTGTGTGACTCAGTCAG 1979
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921 GAAAAAAGTTGTTATTGTCTGTGCATAAGTAAGTGTGTCATAAGTAAGTGTGTGACTCAGTCAG 1980

Qy 1980 ACCCTTTAATGCTGGTCATGTGTAATAATATTGCAAGTAGTAGTAAGAAAACCAAGGTGTCAAGT 2039
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1981 ACCCTTTAATGCTGGTCATGTGTAATAATATTGCAAGTAGTAGTAAGAAAACCAAGGTGTCAAGT 2040

Qy 2040 GTACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTT 2099
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2041 GTACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTT 2100

Qy 2100 CTTTGTGAGAACTTGCATTATTGTCTCCCCAGTAATATTGTTTGGCATCGTGTAGGTCTTTCTTAA 2159
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101 CTTTGTGAGAACTTGCATTATTGTCTCCCCAGTAATATTGTTTGGCATCGTGTAGGTCTTTCTTAA 2160

Qy 2160 TGCTGTGTACCTGCCTCTGCCCACTGTATGGCATCGTGTTATGCTAAAGTTTTTCTTGT 2219
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2161 TGCTGTGTACCTGCCTCTGCCCACTGTATGGCATCGTGTTATGCTAAAGTTTTTCTTGT 2220

Qy 2220 ACATGAAACCCTGGAAACCTACTACACAAAAAACTGTTGTTTCGGCCCCATAGCAGGTGA 2279
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2221 ACATGAAACCCTGGAAACCTACTACACAAAAAACTGTTGTTTCGGCCCCATAGCAGGTGA 2280

Qy 2280 ACTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAG 2339
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2281 ACTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAG 2340

Qy 2340 TTGTTTACCATTATTCAAAGCTCAAAATAGAATTGAAGCCCTCACAAAATCTGTGAT 2399
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2341 TTGTTTACCATTATTCAAAGCTCAAAATAGAATTGAAGCCCTCACAAAATCTGTGAT 2400

Qy 2400 TAATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCACCATAAAACCAGCCATATT 2459
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2400
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Db  2426  TGTATGTGTGCGTGTGATCTCATCCCTCAAGCCTACCTACCATAAAACCAGGCTCA  252485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1617  GAGACCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAA  1676
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252486  GAGACCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAA  252545
Qy  1677  ACCTTACAAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGG  1736
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252546  ACCTTACAAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGG  252605
Qy  1737  TGAGGAACCACTGCTGTTGTCTGTTGTCTGTTGTTCCTGGGAGGGAGGGGTCAGG  1796
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252606  TGAGGAACCACTGCTGTTGTCTGTTGTCTGTTGTTCCTGGGAGGGAGGGGTCAGG  252665
Qy  1797  TGGGAAAGGGCATTAAGATGTTATTGGACAGTTATTGGACAGTTATTGGGTGTTTTT  1856
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252666  TGGGAAAGGGCATTAAGATGTTATTGGACAGTTATTGGACAGTTATTGGGTGTTTTT  252725
Qy  1857  CTAAAATTCACAGGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAA  1916
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252726  CTAAAATTCACAGGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAA  252785
Qy  1917  GGAGAAAAAAGTTGTATTGTCTGTGCATAGTAAGTTGTAGGTGACTGAGAGACTCAGT  1976
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252786  GGAGAAAAAAGTTGTATTGTCTGTGCATAGTAAGTTGTAGGTGACTGAGAGACTCAGT  252845
Qy  1977  CAGACCCTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGAAGAAGGTGTCA  2036
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252846  CAGACCCTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGAAGAAGGTGTCA  252905
Qy  2037  AGTGTACTGCTGGGCAGCGAGGTGATCATTACCAAAGTAATCAACTTGTGGGTGGAGA  2096
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252906  AGTGTACTGCTGGGCAGCGAGGTGATCATTACCAAAGTAATCAACTTGTGGGTGGAGA  252965
Qy  2097  GTTCTTGTGTGAGAACTTGCATTATTTGTGTCCTCCCCTCATGTGTAGGTAGACATTTCT  2156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252966  GTTCTTGTGTGAGAACTTGCATTATTTGTGTCCTCCCCTCATGTGTAGGTAGAACATTTCT  253025
Qy  2157  TAATGCTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTATGTTGGCATCTGTATGTT  2216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253026  TAATGCTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTATGTTGGCATCTGTAAAGTT  253085
Qy  2217  TGTACATGAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCATAGCAGG  2276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253086  TGTACATGAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCATAGCAGG  253145
Qy  2277  TGAACTCATTTTGTGCTTTAATGAAGACAAAATCCACCCCAGTAATATTGCCCTTACG  2336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253146  TGAACTCATTTTGTGCTTTAATGAAGACAAAATCCACCCCAGTAATATTGCCCTTACG  253205
Qy  2337  TAGTTGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCTCCACAAAATCTGT  2396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253206  TAGTTGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCTCCACAAAATCTGT  253265
Qy  2397  GATTAATTTGCTTAATTAGAGCTTCTAATTAGAGCTTCATCCCTCAGCCTACCCTACCAT  2456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253266  GATTAATTTGCTTAATTAGAGCTTCTAATTAGAGCTTCATCCCTCAGCCTACCCATCCAGCCAT  253325
Qy  2457  ATTACTGATACTGTTCAGTGCATTTGAGTGCATTTGAGTAAGTGAGATCC  2516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253326  ATTACTGATACTGTTCAGTGCATTTGAGTGCATTTGAGTAAGTGAGATCC  253385
Qy  2517  AAGCAGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACT  2576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253386  AAGCAGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACT  253445
Qy  2577  ACTTTTCTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACA  2636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  253446  ACTTTTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACA  253505
Qy  2637  TATTTTAAGATAATAGCATAAAGACTTAAAAATGTTCCTCCCCTCCATCTTCCCACACC  2696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2401  TAATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAACCAGGCTCA  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2460  ACTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAG  2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  ACTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAG  2520
Qy  2520  CAGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACT  2579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACT  2580
Qy  2580  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATAT  2639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATAT  2640
Qy  2640  TTTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCTCCATCTTCCCACCCAG  2699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TTTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCTCCATCTTCCCACCCCAG  2700
Qy  2700  TCACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTGTTATTGAGGCTGTTGCT  2759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  TCACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTGTTATTGAGGCTGTTGCT  2760
Qy  2760  TTTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTGGTTTA  2809
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTGGTTTA  2810
```

RESULT 6
US-09-949-016-17189
; Sequence 17189, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17189
; LENGTH: 255679
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255679)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17189

Query Match   50.9%; Score 1433; DB 4; Length 255679;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  1377  TCTCCTTCAGCCTCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAAACTCCAAAACA  1436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252224  TCTCCTTCAGCCTCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAAACTCCAAAACA  252305
Qy  1437  ATCTGACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCAAAGAGCCC  1496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252306  ATCTGACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCC  252365
Qy  1497  TATCTCTATATTTAAGTGTGTGATTGTATTCCATGTGTATATGTGAGTGTGTGTGTG  1556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  252366  TATCTCTATATTTTAAGTGTGTGATTGTATTCCATGTGTATATGTGAGTGTGTGTGTG  252425
Qy  1557  TGTATGTGTGCGTGTGATCTCATCCCTCATAAAAACAGGAGGACTTGAAGACACTTTGGCTCA  1616
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RESULT 7
US-09-643-597-332
; Sequence 332, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Fan, Liqun
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Hosken, Nancy
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Li, Samuel X.
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-332

Query Match   48.9%; Score 1376; DB 3; Length 2270;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT 60

Qy   61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAACCCAGCACACAATGACATCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAACCCAGCACACAATGACATCC 120

Qy   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAAATGAATTCCTCAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAAATGAATTCCTCAGT 180

Qy   181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCTCAGTTCAGTTCAGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCTCAGTTCAGTTCAGCCC 240

Qy   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAGAGATGTGCGACAAACAAGATTGAGATT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAGAGATGTGCGACAAACAAGATTGAGATT 300

Qy   301 AGCATGGAACTGTATCCGGTATCCGAACATGGAGCGCTCCTCGTCCACC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGCATGGAACTGTATCCGGTATCCGAACATGGAGCGCTCCTCGTCCACC 360

Qy   361 ACGAACCTGGGGCTCCTGAACAGCATGACGACCAGCGAGATTCAGAACGGCTCCTCGTCCACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGAACCTGGGGCTCCTGAACAGCATGACGACCAGCGAGATTCAGAACGGCTCCTCGTCCACC 420

Qy   421 AGTCCCTATAAACACAGACCACGCGCAGAACAGCGTCACGCGCCCTCCGCGCCTACGCACAG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   421 AGTCCCTATAAACACAGACCACGCGCAGAACAGCGTCACGCGCCCTCCGCGCCTACGCACAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 CCAGCTCCACCTTCGATGCTCTCGATGCTCTCCATCCACAACAACACCACCCCAACACCGACTAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCAGCTCCACCTTCGATGCTCTCGATGCTCTCCATCCACAACAACACCACCCCAACACCGACTAC 540

Qy   541 CCAGGCCCGCACAGTTCCTTCCAGCAGTCGAGCAGTCGAGCAGTCCCAAGTCGGCCACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCAGGCCCGCACAGTTCCTTCCAGCAGTCGAGCAGTCGAGCAGTCCCAAGTCGGCCACC 600

Qy   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGAACATGCCCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGAACATGCCCATC 660

Qy   661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTGTCTAC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTGTCTAC 720

Qy   721 AAAAAAGTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAAAAAGTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780

Qy   781 GAATTCAACGAGGACAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAATTCAACGAGGACAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGC 840

Qy   841 CATGCCCCAGTATGTAGAAGATCCCATCACAGGAGACAGAGTGTGCTGCTGGTACCTTATGAG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CATGCCCCAGTATGTAGAAGATCCCATCACAGGAGACAGAGTGTGCTGCTGGTACCTTATGAG 900

Qy   901 CCACCCCAGGTTGCACTGAATTCAGTCTTGTACACAGTCATGTGTAACACAGCAGT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCACCCCAGGTTGCACTGAATTCAGTCTTGTACACAGTCATGTGTAACACAGCAGT 960

Qy   961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT 1020

Qy 1021 GGGCAAGTCCTGGGCCGACGCTGCTTGAGGCCCGGATCGTGCTGTCGTGCGTTGCCCAGGAGAGAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGGCAAGTCCTGGGCCGACGCTGCTTGAGGCCCGGATCGTGCTGTCGTGCGTTGCCCAGGAGAGAC 1080

Qy 1081 AGGAAGGCGGATGAAGATAGCATCAGAAGCAGCAAGTTTCGGACAGCAGTACAAAGAACGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 AGGAAGGCGGATGAAGATAGCATCAGAAGCAGCAAGTTTCGGACAGCAGTACAAAGAACGT 1140

Qy 1141 GATGGTACGAGAGGCGCCGTTTCGTCAGAACAACACATGACATCCATCAAG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GATGGTACGAGAGGCGCCGTTTCGTCAGAACAACACATGACATCCATCAAG 1200

Qy 1201 AAACGAAGATCCCAGATGATGAACGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AAACGAAGATCCCAGATGATGAACGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy 1261 GAAATGCGTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGCTCCTTCCTCAGCACACA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GAAATGCGTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGCTCCTTCCTCAGCACACA 1320

Qy 1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCAACAGCACTTACTTCAGAAACA 1376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCAACAGCACTTACTTCAGAAACA 1376

RESULT 8
US-09-542-615A-332
; Sequence 332, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Fan, Liqun
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Bangur, Chaitanya S.

Db 253506 TATTTTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCTCCATCTTCCACACC 253565
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2697 CAGTCACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTGTTATTGAGGCTGTT 2756
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253566 CAGTCACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTGTTATTGAGGCTGTT 253625

Qy   2757 GCTTTTGTGGATGTGTGATTTAATTTTCAATAAACTTTTGCATCTTGTTTA 2809
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253626 GCTTTTGTGGATGTGTGATTTAATTTTCAATAAACTTTTGCATCTTGTTTA 253678

; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-332

Query Match 48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT   60

Qy   61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120

Qy 121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180

Qy 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGAACCATCAGAGATGTTCAGTTCAGCCC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGAACCATCAGAGATGTTCAGTTCAGCCC 240

Qy 241 ATTGACTTGTGTGATGAACCATCAGAGAGATGGTGCGACAAACAAGATTGAGATT   300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATTGACTTGTGTGATGAACCATCAGAGAGATGGTGCGACAAACAAGATTGAGATT   300

Qy 301 AGCATGGACTGTATCCGCAGGACTCGGACCTCGAGTGACCCATGTGGCCACAGTAC   360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 AGCATGGACTGTATCCGCAGGACTCGGACCTCGAGTGACCCATGTGGCCACAGTAC   360

Qy 361 ACGAACCTGGGGCTCCTGAACAGCAGCCAGCAGATTCAGAACGGCTCCTCGTCCACC   420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 ACGAACCTGGGGCTCCTGAACAGCAGCCAGCAGATTCAGAACGGCTCCTCGTCCACC   420

Qy 421 AGTCCCTATAAACACAGACCACGCGGCAGAACAGGGTCACGGCGCCCTCACGCACACAG   480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 AGTCCCTATAAACACAGACCACGCGGCAGAACAGGGTCACGGCGCCCTCACGCACACAG   480

Qy 481 CCCAGCTCCACCTTGATGCTCTCTCTCCATCACCGGACTCCAACACCGACTAC   540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 CCCAGCTCCACCTTGATGCTCTCTCTCCATCACCGGACTCCAACACCGACTAC   540

Qy 541 CCAGGCCCGCACAGTTTCGACGTGTCCTTCCAGCAGTCGAGCAGTCGGCCACC   600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CCAGGCCCGCACAGTTTCGACGTGTCCTTCCAGCAGTCGAGCAGTCGGCCACC   600

Qy 601 TGGACGTATTCCACTGAACTGAAGAAACTTCTACTGCCAAATTGCAAAGACACATGCCCCATC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 TGGACGTATTCCACTGAACTGAAGAAACTTCTACTGCCAAATTGCAAAGACACATGCCCCATC 660

Qy 661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTTATCCCGCCATGCCTGTCTAC   720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTTATCCCGCCATGCCTGTCTAC   720

Qy 721 AAAAAAGCTGAGCACGTCACGGAGGTGTGAAGCGGTGGTGCACCGGT   780
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 721 AAAAAAGCTGAGCACGTCACGGAGGTGTGAAGCGGTGGTGCACCGGT   780

Qy 781 GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCGAGTAGAGGGGAACAGC   840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCGAGTAGAGGGGAACAGC   840

Qy 841 CATGCCCCAGTATGTAGAAGATCCCATCACAGGAGACAGAGTGTGTCGGTACCTTATGAG   900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 CATGCCCCAGTATGTAGAAGATCCCATCACAGGAGACAGAGTGTGTCGGTACCTTATGAG   900

Qy 901 CCACCCCAGGTTGGCACTGCAATTCACGACACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 CCACCCCAGGTTGGCACTGCAATTCACGACACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy 961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATGTTACTCTGGAAACCAGAGAT   1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATGTTACTCTGGAAACCAGAGAT   1020

Qy 1021 GGGCAAGTCCTGGGCCGACGCTGCTTTGAGGCCCGGATCTGCTTGCCCCAGGAAGAGAC   1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGGCAAGTCCTGGGCCGACGCTGCTTTGAGGCCCGGATCTGCTTGCCCCAGGAAGAGAC   1080

Qy 1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAGAGTTCGACAGTACAAAGAAACGGT   1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAGAGTTCGGCAGTACAAAGAAACGGT   1140

Qy 1141 GATGGTACGAAGCCCCGTTTCGTCAGAACACACATGGTATCCGAGATGACATCCATCAAG 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GATGTACGAAGCGCCCGTTTCGTCAGAACACACATGGTATCCGAGATGACATCCATCAAG 1200

Qy 1201 AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGCCGTGAGACTTAT   1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGCCGTGAGACTTAT   1260

Qy 1261 GAAATGTCTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGCCAGCAGCACCACACA   1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GAAATGTCTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGCCAGCAGCACCACACA   1320

Qy 1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCAGCAGCAGCACCACTTACTTCAGAAACA 1376
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCAGCAGCAGCACCACTTACTTCAGAAACA 1376

RESULT 9
US-09-606-421B-332
; Sequence 332, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-332

Query Match 48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1376; Conservative 0;

Qy   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT   60

```
Qy   1141 GATGGTACGAAGGCGCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGGTACGAAGGCGCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200

Qy   1201 AAACGAAGATCCCAGATGATGAACTGTTATATTACCAGTGAGGGGCCGTGAGACTTAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAACGAAGATCCCAGATGATGAACTGTTATATTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy   1261 GAAATGCTGTTGAAGATCAAAGAGTCCTGGAACTCATGCAGTCCTCCGACACACA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAATGCTGTTGAAGATCAAAGAGTCCTGGAACTCATGCAGTCCTCCGACACACA 1320

Qy   1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376
```

RESULT 10
US-09-630-940B-332
; Sequence 332, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND.DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-332

Query Match   48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT 60

Qy     61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120

Qy    121 AAAGAAAGTTATTACCGATCCACCATGTGCCGCACACAGACAAATGAATTCCTCAGT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGAAAGTTATTACCGATCCACCATGTGCCGCACACAGACAAATGAATTCCTCAGT 180

Qy    181 CCAGAGGTTTTCCAGCATATCTGGATTTTACTCTGGAAACCAGAGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGAGGTTTTCCAGCATATCTGGATTTTACTCTGGAAACCAGAGAT 240

Qy    241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGTGCGACAAACAAGATTGAGATT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGTGCGACAAACAAGATTGAGATT 300

Qy    301 AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTAGTGGCCACAGTAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTAGTGGCCACAGTAC 360

Qy    301 AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTAGTGGCCACAGTAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTAGTGGCCACAGTAC 360

Qy    361 ACGAACCTGGGGCTCCTGAACAGCATGGAACAGCAGATTCAGACCGCTCCTCCGTCCACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACGAACCTGGGGCTCCTGAACAGCATGGAACAGCAGATTCAGACCGCTCCTCCGTCCACC 420

Qy    421 AGTCCCTATAACACAGACCACGCGCAGAACAGCGTCACGGGCCCTCGCCCTACGCGCACAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTCCCTATAACACAGACCACGCGCAGAACAGCGTCACGGGCCCTCGCCCTACGCGCACAG 480

Qy    481 CCCAGCTCCACCTTCGATGCTTCTCTCCATCACCGCCATCCCCTCCAACACCGACTAC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCCAGCTCCACCTTCGATGCTTCTCTCCATCACCGCCATCCCCTCCAACACCGACTAC 540

Qy    541 CCAGGCCGCACAGTTCGACGTGTCCTTCCAGCAGTGAGCAGTCGGCCAGTCGGCGGCCACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAGGCCGCACAGTTCGACGTGTCCTTCCAGCAGTGAGCAGTCGGCCAGTCGGCGGCCACC 600

Qy    601 TGGACGTATTCCACTGAACTCTACTGCCAAATTGCAAAGAACATGCCCCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGGACGTATTCCACTGAACTCTACTGCCAAATTGCAAAGAACATGCCCCATC 660

Qy    661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCGTGTTATCCGCGCCATGCCTGTCTAC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCGTGTTATCCGCGCCATGCCTGTCTAC 720

Qy    721 AAAAAACTGACCAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAAAAACTGAGCAGCACGTGACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780

Qy    781 GAATTCAACGAGGGACAGATTGCCCCTCTAGTCATTTGATTCGAGTGAGAGGGGAACAGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GAATTCAACGAGGGACAGATTGCCCCTCTAGTCATTTGATTCGAGTGAGAGGGGAACAGC 840

Qy    841 CATGCCCAGTATGTAGAAGATCCATCACAGAGAAGACAGAGAGTGTCGGTGGTACCTTATGAG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGCCCAGTATGTAGAAGATCCATCACAGAGAAGACAGAGAGTGTCGGTGGTACCTTATGAG 900

Qy    901 CCACCCCAGGTTGGCACTGAATTCAGGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCACCCCAGGTTGGCACTGAATTCAGGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy    961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTAATCATTGTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT 1020

Qy   1021 GGGCAAGTCCTGGGCCCGAGCGCTGCTTTGAGGCCCGGATCTGCGTGCTTGCCCAGGAAGAGAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGGCAAGTCCTGGGCCCGAGCGCTGCTTTGAGGCCCGGATCTGCGTGCTTGCCCAGGAAGAGAC 1080

Qy   1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140
```

; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 4849
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-643-597-335

Query Match   48.4%; Score 1364; DB 3; Length 4849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1375; Conservative 0; Mismatches 0; Indels 0; Gaps 1;

Qy   2 CGTTGATATCAAAGACAGTTGAAGAAATGAATTTTGAAACTTCACGGTGTGCCACCCTA 61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGTTGATATCAAAGACAGTTGAAGAAATGAATTTTGAAACTTCACGGTGTGCCACCCTA 60

Qy   62 CAGTACTGCCCTGACCCTTACATCCGATCCACCATGTCCCAGAGCACACAGACAAATTCCTCAGT 120
            ||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   61 CAGTACTGCCCTGACCCTTACATCCGATCCACCATGTCCCAGAGCACACAGACAAATTCCTCAGT 120

Qy   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180

Qy   181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCAGATTTCTGGAACAGCAGCC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCAGATTTCTGGAACAGCAGCC 240

Qy   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGGGACAAAACAAGATTGAGATT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGGGACAAAACAAGATTGAGATT 300

Qy   301 AGCATGGACTGTATCCGCATGGCAGACTCGGACCTCGAGTCGACCCCATGTGGCCACAGTAC 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGCATGGACTGTATCCGCATGGCAGACTCGGACCTCGAGTCGACCCCATGTGGCCACAGTAC 360

Qy   361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC 420

Qy   421 AGTCCCTATAACAGACCACGCGAGAAACAGTCGTCACACCGACTAC 480
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGTCCCTATAACAGACCACGCGAGAAACAGTCGTCACACCGACTAC 480

Qy   481 CCCAGCTCCACCTTCGATGCTCCCTCCTCCCTCCAACACCGACTAC 540
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCAGCTCCACCTTCGATGCTCCCTCCTCCCTCCAACACCGACTAC 540

Qy   541 CCAGGCCCGCACAGTTCGACGTGCTTCCTTCCAGCAGTGCCAAGTCGGCCACC 600
            |||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCAGGCCCGCACAGTTCGACGTGCTTCCTTCCAGCAGTGCCAAGTCGGCCACC 600

Qy   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAATGCCCCATC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAATGCCCCATC 660

Qy   361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC 420

Qy   421 AGTCCCTATAACAGACCACGCGAGAAACAGTCGTCACACCGACTAC 480
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGTCCCTCCACCTTCGATGCTCCCTCCTCCCTCCAACACCGACTAC 480

Qy   481 CCCAGCTCCACCTTCGATGCTCCCTCCTCCCTCCAACACCGACTAC 540
            ||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCAGCTCCACCTTCGATGCTCCCTCCTCCCTCCAACACCGACTAC 540

Qy   541 CCAGGCCCGCACAGTTTCGACGTGCTTCCTTCCAGCAGTGCCAAGTCGGCCACC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCAGGCCCGCACAGTTTCGACGTGCTTCCTTCCAGCAGTGCCAAGTCGGCCACC 600

Qy   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAATGCCCCATC 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAATGCCCCATC 660

Qy   661 CAGATCAAGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGGCCATGCCTGTCTAC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGATCAAGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGGCCATGCCTGTCTAC 720

Qy   721 AAAAAAGTGAGCACGTCACGGAGTGGTGAAGCCGTGCCCAACCATGAGCTGAGCCGT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAAAAAGTGAGCACGTCACGGAGTGGTGAAGCCGTGCCCAACCATGAGCTGAGCCGT 780

Qy   781 GAATTCAACGAGGAGGACAGCAGATTGCCCCTCCAGTCATTTGATTCGAGTAGAGGGGGAACAGC 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAATTCAACGAGGAGGACAGCAGATTGCCCCTCCAGTCATTTGATTCGAGTAGAGGGGGAACAGC 840

Qy   841 CATGCCCAGTATGTAGAGATCCCATCACAGGAAGACAGAGTGTCTGGTACTTATGGGTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CATGCCCAGTATGTAGAGATCCCATCACAGGAAGACAGAGTGTCTGGTACTTATGAGTG 900

Qy   901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy   961 TGTGTTGGAGGGATGAACCGCGTCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGTGTTGGAGGGATGAACCGCGTCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT 1020

Qy   1021 GGGCAAGTCCTGGGCCGACCGTGCTTTGAGCCCCGGATCGTGTGCTTGCCCAGGAAGAGAC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGGCAAGTCCTGGGCCGACCGTGCTTTGAGCCCCGGATCGTGTGCTTGCCCAGGAAGAGAC 1080

Qy   1081 AGGAAGGCCGATGAAGATAGCATCAGAAGCAGAAGTTTCGGACAGTACAAAGAACGGT 1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGGAAGGCCGATGAAGATAGCATCAGAAGCAGAAGTTTCGGACAGTACAAAGAACGGT 1140

Qy   1141 GATGGTACGGAAGCCCCGTTTCGTCAGAACACACATGGTATCCAGATGACACATCCATCAAG 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGGTACGGAAGCCCCGTTTCGTCAGAACACACATGGTATCCAGATGACACATCCATCAAG 1200

Qy   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT 1260

Qy   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAACTTCCTCAGCACACA 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAACTTCCTCAGCACACA 1320

Qy   1321 ATTGAAACGTACAGGCAACAGCAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGAAACGTACAGGCAACAGCAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376

RESULT 11
US-09-643-597-335
; Sequence 335, Application US/09643597

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Query Match        48.4%;  Score 1364;  DB 4;  Length 4849;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1375;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  1;

Qy     2 CGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCTA   61
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     1 CGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCTA   60

Qy    62 CAGTACTGCCCTGACCCTTACATCCAGCTTCGTGAGAAA-CCCAGCTGAGGGGAACAGC  120
         ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    61 CAGTACTGCCCTGACCCTTACATCCAGCTTCGTGAGAAACCCAGCTGAGGGGAACAGC   120

Qy   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT 180

Qy   181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240

Qy   241 ATTGACTTGAACTTGTGTCGGATCTCGTTGCTTGCCCGGACTGGCCATGTGGCCACAGATT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTGACTTGAACTTGTGTCGGATCTCGTTGCTTGCCCGGACTGGCCATGTGGCCACAGATT 300

Qy   301 AGCATGATGAACGTGTATCCGGATCGTGTGCTTTGCGGATCGTGTGCTTGCGGATCGTGTGC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGCATGATGAACGTGTATCCGGATCGTGTGCTTTGCGGATCGTGTGCTTGCGGATCGTGTGC 360

Qy   361 ACGAACTTGGGGCGGATGAAGATAGCAGCAAGTTTCGGACAGTACAAAGAACGGT      420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGAACTTGGGGCGGATGAAGATAGCAGCAAGTTTCGGACAGTACAAAGAACGGT      420

Qy   421 AGTCCTATAACAGAGCGCCCGTTTCGTTCGTCAGAACACACATGTATCCATCCATCAAG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGTCCTATAACAGAGCGCCCGTTTCGTTCGTCAGAACACACATGTATCCATCCATCAAG  480

Qy   481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGATGGGGCCGTGAGGGGCGTGACTTAT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGATGGGGCCGTGAGGGGCGTGACTTAT 540

Qy   541 CCAGGCCCGCACAGTTCGATGGGGCCAAGAGTCCCTGGAACTCATGCAGTCCTCAGCACACA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCAGGCCCGCACAGTTCGATGGGGCCAAGAGTCCCTGGAACTCATGCAGTCCTCAGCACACA 600

Qy   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCAAGAGATCCCATCGCCCCATC     660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCAAGAGATCCCATCGCCCCATC     660

Qy   661 CAGATCAAGGTGATGACCCCACCTTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGATCAAGGTGATGACCCCACCTTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC 720

Qy   721 AAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT  780

Qy   781 GAATTCAACGAGGGGACAGATTGCCCCTCCAGTCATTGATTCGAGTAGAGGGGAACAGC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAATTCAACGAGGGGACAGATTGCCCCTCCAGTCATTGATTCGAGTAGAGGGGAACAGC 840

Qy   841 CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGGTACCTTATGAG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGGGTACCTTATGAG 900

Qy   901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy   961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT 1020

Qy  1021 GGGCAAGTTCCTGGCCGACGCTGTGCTTTGAGGGCCGGATCGTGTGCTTGCCCGGATCGTGTGCTTGCCCGGAGAAGAGAC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGGCAAGTTCCTGGCCGACGCTGTGCTTTGAGGGCCGGATCGTGTGCTTGCCCGGAGAAGAGAC 1080

Qy  1081 AGGAAGGCGGATGAAGATAGCAGCAAGTTTCGGACAGTACAAAGAACGGT        1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGGAAGGCGGATGAAGATAGCAGCAAGTTTCGGACAGTACAAAGAACGGT        1140

Qy  1141 GATGGTACGAAGGCCCGTTCGTCAGAACACACATGTATCCAGATGACATCCATCAAG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GATGGTACGAAGGCCCGTTCGTCAGAACACACATGTATCCAGATGACATCCATCAAG 1200

Qy  1201 AAACGAAGATCCCCAGATGATGAAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AAACGAAGATCCCCAGATGATGAAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy  1261 GAAATGCTGTTGAAGATCACAGGCAACAGCAGCAGCAACAGCAGCCACTTACTTCAGAAACA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GAAATGCTGTTGAAGATCACAGGCAACAGCAGCAGCAACAGCAGCCACTTACTTCAGAAACA 1320

Qy  1321 ATTGAAACGTACAGGCAACAGCAGCAGCAACAGCAGCCACTTACTTCAGAAACA 1376
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATTGAAACGTACAGGCAACAGCAGCAGCAACAGCAGCCACTTACTTCAGAAACA 1376
```

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Qy   1021 GGGCAAGTCCTGGGCCGACGCGTGCTTTGAGGCCGATCTGTGCTTGCCCAGGAAGAGAC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGGCAAGTCCTGGGCCGACGCGTGCTTTGAGGCCGATCTGTGCTTGCCCAGGAAGAGAC 1080

Qy   1081 AGGAAGGCGGATGAAGATAGCAGCATCAGAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGGAAGGCGGATGAAGATAGCAGCATCAGAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140

Qy   1141 GATGGTACGGAGGCGCCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGGTACGGAGGCGCCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200

Qy   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTACTTCCTCAGCACACA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTACTTCCTCAGCACACA 1320

Qy   1321 ATTGAAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGAAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376
```

RESULT 13
US-09-606-421B-335

; Sequence 335, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-335

Query Match   48.4%; Score 1364; DB 4; Length 4849;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1375; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy      2 CGTTGATATCAAAGACAGTTGAAGGAAAATGAATTTGAAACTTCACGGTGTGCCACCCTA 61
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      1 CGTTGATATCAAAGACAGTTGAAGGAAAATGAATTTGAAACTTCACGGTGTGCCACCCTA 60

Qy     62 CAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAA--CCAGTCATTTCTTCTTGG 120
          ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db     61 CAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCCAGTCATTTCTTCTTGG 120

Qy    121 AAAGAAAGTTATTACCGATCTCCACCATGTCCAGAGCACACAAATGAATTCCTCAGT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGAAAGTTATTACCGATCTCCACCATGTCCAGAGCACACAAATGAATTCCTCAGT 180

Qy    181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240

Qy    241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT 300
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Db    241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT 300

Qy    301 AGCATGGCCGTATCCGATCCGGACTCGGACTCGGACTCGGCCACGACCCCATGTGGCCACAGTAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGCATGGCCGTATCCGATCCGGACTCGGACTCGGACTCGGCCACGACCCCATGTGGCCACAGTAC 360

Qy    361 ACGAACCTGGGCTCCTGAACAGCAGCATGGACCAGATTCAGAACGTCAGAACGGCTCCTCGTCCACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACGAACCTGGGCTCCTGAACAGCAGCATGGACCAGATTCAGAACGTCAGAACGGCTCCTCGTCCACC 420

Qy    421 AGTCCCTATAACACAGACACGCGCGAGAACAGCGTCACGCGGCCCCTCACGCACGCAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTCCCTATAACACAGACACGCGCGAGAACAGCGTCACGCGGCCCCTCACGCACGCAG 480

Qy    481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCCCGCCATCCCTCCAACACCGACTAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCCAGCTCCACCTTCGATGCTCTCTCCATCACCCCGCCATCCCTCCAACACCGACTAC 540

Qy    541 CCAGGGCCGACAGTTTCGACGTGTCCTTCAGCAGTCGAGCACTCGGCCACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAGGGCCGACAGTTTCGACGTGTCCTTCAGCAGTCGAGCACTCGGCCACC 600

Qy    601 TGGACGTATTCCACTGAACTGAAGAAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC 660
          |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGGACGTATTCCACTGAACTGAAGAAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC 660

Qy    661 CAGATCAAGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGGCCGCTGTTATCCGGCCGTGTCTAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAGATCAAGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGGCCGCTGTTATCCGGCCGTGTCTAC 720

Qy    721 AAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780

Qy    781 GAATTCAACGGACGACGATTGCCCCTCCAGTCATTGAATTCGAGTAGAGGGAACAGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GAATTCAACGGACGACGATTGCCCCTCCAGTCATTGAATTCGAGTAGAGGGAACAGC 840

Qy    841 CATGCCCAGTATGTGGACTGAAGATCCCATCACAGGAGAACAGAGTGTGCTGGTACCTTATGAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGCCCAGTATGTGGACTGAAGATCCCATCACAGGAGAACAGAGTGTGCTGGTACCTTATGAG 900

Qy    901 CCACCCCCAGGTTGGCACTGAATTCACGACACTCTGACAATTCATGTGTAACAGCAGT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCACCCCCAGGTTGGCACTGAATTCACGACACTCTGACAATTCATGTGTAACAGCAGT 960

Qy    961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
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Db   1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376


RESULT 14
US-09-630-940B-335
; Sequence 335, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Fan, Liqun
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Hosken, Nancy
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Li, Samuel X.
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: McNeill, Patricia D.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.455C10
;   CURRENT APPLICATION NUMBER: US/09/630,940B
;   CURRENT FILING DATE: 2000-08-02
;   NUMBER OF SEQ ID NOS: 367
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 4849
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-630-940B-335

Query Match       48.4%;   Score 1364;  DB 4;  Length 4849;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1375;   Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

Qy    2 CGTTGATATCAAAGACAGTTGAAGAAATGAATTTGAAACTTCACGGTGTGCCACCCTA   61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CGTTGATATCAAAGACAGTTGAAGAAATGAATTTGAAACTTCACGGTGTGCCACCCTA   60

Qy   62 CAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAA-CCCAGCTCATTTCTCTTGG  120
         |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   61 CAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCCAGCTCATTTCTCTTGG  120

Qy  121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGAGCAAATGAATTCCTCAGT  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGAGCAAATGAATTCCTCAGT  180

Qy  181 CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240

Qy  241 ATTGACTTGAACTTGTGTGATGAACCATCAGAAGATGTGCGACAAACAAGATTGAGATT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATTGACTTGAACTTGTGTGATGAACCATCAGAAGATGTGCGACAAACAAGATTGAGATT  300

Qy  301 AGCATGGACTGTATCCGCAGGACTCGGACCTCGGACGTCGAGTGGCCACAGTAC  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGCATGGACTGTATCCGCAGGACTCGGACCTCGGACGTCGAGTGGCCACAGTAC  360

Qy  361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420

Qy  421 AGTCCCTATAAACAGACAACAGGCTCACGGCCGCCCTCGCCCTACGCACAG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AGTCCCTATAAACAGACAACAGGCTCACGGCCGCCCTCGCCCTACGCACAG  480

Qy  481 CCCAGCTCCACCTTCGATGCTCTGCTCTCTCCATCACCCGGCATCCCCAAACACCGACTAC  540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCCAACACCGACTAC  540

Qy  541 CCAGGCCCGCACAGTTCCTTCCAGCGTGTCCTTCCAGCAGTCGAGCGTCGGCCACC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 CCAGGCCCCACCAGTTCGACGTGTCCTTCCAGCAGTCGAGCAGTCGGCCACC  600

Qy  601 TGGACGTATTCCACTGAACTGAAGAAACTTCACTGCCAAATTGCAAAGACATGCCCCATC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TGGACGTATTCCACTGAACTGAAGAAACTTCACTGCCAAATTGCAAAGACATGCCCCATC  660

Qy  661 CAGATCAAGTGATGACCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CAGATCAAGTGATGATGACCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720

Qy  721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGGGGTGCCCAACCATGAGCTGAGCCGGT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGGGGTGCCCAACCATGAGCTGAGCCGGT  780

Qy  781 GAATTCAACGAGGGACAGAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGAACAGC  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GAATTCAACGAGGGACAGAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGAACAGC  840

Qy  841 CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTAGGTACCTTATGAG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTAGGTACCTTATGAG  900

Qy  901 CCACCCCAGGTTGGCCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAAACAGCAGT  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 CCACCCCAGGTTGGCCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAAACAGCAGT  960

Qy  961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTTCTGGAAACCAGAGAT 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTTCTGGAAACCAGAGAT 1020

Qy 1021 GGGCAAGTCCTGGGCCGACGCTGCTTTGAGGCCCGGATCGTGCTTGCCCAGGAAGAGAC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGGCAAGTCCTGGGCCGACGCTGCTTTGAGGCCCGGATCGTGCTTGCCCAGGAAGAGAC 1080

Qy 1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT 1140

Qy 1141 GATGGTACGGAAGCGCCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 GATGGTACGGAAGCGCCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200

Qy 1201 AAACGAAGATCCCCAGATGATGAACGTGTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 AAACGAAGATCCCCAGATGATGAACGTGTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy 1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA 1320

Qy 1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACA 1376


RESULT 15
US-09-643-597-337
; Sequence 337, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Fan, Liqun
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Hosken, Nancy
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Li, Samuel X.
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: McNeill, Patricia D.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

```
; TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE:  210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE:  2000-08-21
; NUMBER OF SEQ ID NOS:  369
; SOFTWARE:  FastSEQ for Windows Version 3.0
SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-337

Query Match           43.8%;  Score 1232;  DB 3;  Length 1551;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1232;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 60

Qy     205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGTGTGGATGAA 264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGTGTGGATGAA 120

Qy     265 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGCATGGACTGTATCCGCATGCAG 324
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Db     121 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGCATGGACTGTATCCGCATGCAG 180

Qy     325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC 384
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Db     181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC 240

Qy     385 ATGGACCAGCAGATTCAGAACGGCGCCTCCTGCCACCAGTCCCTATAACACAGACCACGCG 444
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Db     241 ATGGACCAGCAGATTCAGAACGGCGCCTCCTGCCACCAGTCCCTATAACACAGACCACGCG 300

Qy     445 CAGAACAGCGCTCACGGCGCCCTCGCCCTACGGCACAGCACAGCCCAGCTCCACCTTCGATGCTCTC 504
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Db     301 CAGAACAGCGCTCACGGCGCCCTCGCCCTACGGCACAGCACAGCCCAGCTCCACCTTCGATGCTCTC 360

Qy     505 TCTCCATCACCCGCCATCCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG 564
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Qy     565 TCCTTCCAGCAGTCGAGCACCACGGCACCGCGCCAAGTCGGCGACGTATTCCACTGAACTGAAG 624
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Qy     625 AAACTCTACTGCCAAATTGCAAAGACATGCCCATCCAGATCCAGATCAAAAAAGCTGAGCAGGTGACCCCACCT 684
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Qy     685 CCTCAGGGAGCTGTTATCGCGCGCCATGCCATGCCTGTCTTACAAAAAAGCTGAGCACGTGCACGGAG 744
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Qy     745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAGCCGTGAATTCAACGAGGACACAGATTGCC 804
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Qy     925 ACGACAGTCTTGTACAAATTCATGTGTAACAGCAGTAGTTGTGTTGGAGGGATGAACCGCCGT 984
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Search completed: October  3, 2005, 09:27:59
Job time : 459 secs
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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: October 3, 2005, 06:01:58 ; Search time 936 Seconds
(without alignments)
3304.793 Million cell updates/sec.

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Scoring table: BLOSUM62
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Delop 6.0 , Delext 7.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Database : Published_Applications NA:*
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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2383	100.0	1347	19	US-10-716-359-3	Sequence 3, Appli
2	2383	100.0	2816	9	US-09-735-705-333	Sequence 333, App
3	2383	100.0	2816	9	US-09-850-716A-333	Sequence 333, App
4	2383	100.0	2816	9	US-09-897-778-333	Sequence 333, App
5	2383	100.0	2816	14	US-10-007-700-333	Sequence 333, App
6	2383	100.0	2816	15	US-10-117-982-333	Sequence 333, App
7	2383	100.0	2816	16	US-10-393-590-26	Sequence 26, Appl
8	2383	100.0	2816	16	US-10-393-590-27	Sequence 27, Appl
9	2383	100.0	2816	16	US-10-393-590-64	Sequence 64, Appl
10	2383	100.0	2816	16	US-10-393-590-65	Sequence 65, Appl
11	2383	100.0	2816	16	US-10-393-567-26	Sequence 26, Appl
12	2383	100.0	2816	16	US-10-393-567-27	Sequence 27, Appl
13	2383	100.0	2816	16	US-10-393-567-64	Sequence 64, Appl
14	2383	100.0	2816	16	US-10-393-567-65	Sequence 65, Appl
15	2383	100.0	2816	16	US-10-394-087-26	Sequence 26, Appl
16	2383	100.0	2816	16	US-10-394-087-27	Sequence 27, Appl
17	2383	100.0	2816	16	US-10-394-087-64	Sequence 64, Appl
18	2383	100.0	2816	16	US-10-394-087-65	Sequence 65, Appl
19	2383	100.0	2816	17	US-10-311-986-333	Sequence 333, App
20	2383	100.0	2816	20	US-10-775-972-333	Sequence 333, App
21	2383	100.0	2816	22	US-10-922-124-333	Sequence 333, App
22	2296	96.3	1452	19	US-10-716-359-9	Sequence 9, Appli
23	2185	91.7	1551	9	US-09-735-705-337	Sequence 337, App
24	2185	91.7	1551	9	US-09-850-716A-337	Sequence 337, App
25	2185	91.7	1551	9	US-09-897-778-337	Sequence 337, App
26	2185	91.7	1551	14	US-10-007-700-337	Sequence 337, App
27	2185	91.7	1551	15	US-10-117-982-337	Sequence 337, App
28	2185	91.7	1551	17	US-10-311-986-337	Sequence 337, App
29	2185	91.7	1551	19	US-10-716-359-2	Sequence 2, Appli
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32	2185	91.7	1926	19	US-10-716-359-1	Sequence 1, Appli
33	2185	91.7	2270	9	US-09-735-705-332	Sequence 332, App
34	2185	91.7	2270	9	US-09-850-716A-332	Sequence 332, App
35	2185	91.7	2270	9	US-09-897-778-332	Sequence 332, App
36	2185	91.7	2270	14	US-10-007-700-332	Sequence 332, App
37	2185	91.7	2270	15	US-10-117-982-332	Sequence 332, App
38	2185	91.7	2270	17	US-10-313-986-332	Sequence 332, App
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41	2185	91.7	4849	9	US-09-735-705-335	Sequence 335, App
42	2185	91.7	4849	9	US-09-850-716A-335	Sequence 335, App
43	2185	91.7	4849	9	US-09-897-778-335	Sequence 335, App
44	2185	91.7	4849	14	US-10-007-700-335	Sequence 335, App
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ALIGNMENTS

RESULT 1
US-10-716-359-3
; Sequence 3, Application US/10716359
; Publication No. US20040132120A1
; GENERAL INFORMATION:
; APPLICANT: McKeon, Frank
; APPLICANT: Yang, Annie
; TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
; TITLE OF INVENTION: RELATED THERETO
; FILE REFERENCE: HMV-038.01
; CURRENT APPLICATION NUMBER: US/10/716,359
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/09/174,493
; PRIOR FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/087,216
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29

Pred. No. is the number of results predicted by chance to have a

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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/062,076
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1344)
US-10-716-359-3

Alignment Scores:
Pred. No.:       3.81e-277        Length:              1347
Score:           2383.00          Matches:             448
Percent Similarity: 100.00%       Conservative:        0
Best Local Similarity: 100.00%    Mismatches:          0
Query Match:     100.00%          Indels:              0
DB:                               Gaps:                19

US-09-670-568C-1 (1-448) x US-10-716-359-3 (1-1347)
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Qy   101  GlnAsnSerValThrArgAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu   120
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Db   841  CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC   900

Qy   301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgThrGluGluGluAsnSerIle   320
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; Sequence 333, Application US/09735705
; Patent No. US2002005232929A1
; GENERAL INFORMATION:
; APPLICANT:  Wang, Tongtong
; APPLICANT:  Fan, Liqun
; APPLICANT:  Kalos, Michael D.
; APPLICANT:  Bangur, Chaitanya S.
; APPLICANT:  Hosken, Nancy
; APPLICANT:  Fanger, Gary R.
; APPLICANT:  Li, Samuel X.
; APPLICANT:  Wang, Aijun
; APPLICANT:  Skeiky, Yasir A.W.
; APPLICANT:  Henderson, Robert A.
; APPLICANT:  McNeill, Patricia D.
; APPLICANT:  Fanger, Neil
; TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE:  210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE:  2000-12-12
; NUMBER OF SEQ ID NOS:  419
; SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-333

Alignment Scores:
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Pred. No.:                        Length:        2816
Score:                 1.21e-276  Matches:       448
Percent Similarity:    2383.00    Conservative:  0
Best Local Similarity: 100.00%    Mismatches:    0
Query Match:           100.00%    Indels:        0
DB:                               Gaps:          9

US-09-670-568C-1 (1-448) x US-09-735-705-333 (1-2816)

Qy    1  MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATGTCCCAGAGCACCCAGACCAACGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG
Db  145  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  204

Qy   21  AspPheLeuGluGluCysSerValGlnProIleLeuAspLeuAsnPheValAspGlu     40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GATTTTCTGGAACAGCTATATGTTCAGTTCAGCCCATTGAACTTTGTGGATGAA
Db  205  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  264

Qy   41  ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG
Db  265  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  324

Qy   61  AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GACTCCGACCTGAGTGACCCCATGTGGCCACAGTACACCAACCTGGGCTCCTGAACAGC
Db  325  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  384

Qy   81  MetAspGlnIleLeuGlnAsnGlySerSerThrSerProTyrAsnThrAspHisAla    100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATGGACCAGATTCAGAACGGCTCCTCCACCAGTCCCTATAACACAGACCACGCG
Db  385  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  444

Qy  101  GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerProPheAspAlaLeu  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCTCACCTTCGATGCTCTC
Db  445  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  504

Qy  121  SerProSerProAlaIleProSerArgAsnThrAspTyrProGlyProHisSerPheAspVal  140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TCTCCATCACCCGCCATCCCTTCCACAACCGACTACCCAGGCCCCACAGTTTCGACGTG
Db  505  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  564

Qy  141  SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTrpSerThrGluLeuLys    160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TCCTTCCAGCAGTCGAGCACCGCCAAGTCGGCCACCTGGACCTATTCCACTGAACTGAAG
Db  565  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  624

Qy  161  LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysLysValMetProPro  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AAACTTACTGCCAAATTGCAAATGATGCCCCATCCAGATCAAGGTGATGACCCCCACCT
Db  625  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  684

Qy  181  ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG
Db  685  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  744

Qy  201  ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTGGTGAAGCGGTGCCCCAACCATGAACTGAGCCGTGAATTCAACGAGGGACAGATTGCC
Db  745  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  804

Qy  221  ProProSerHisLeuIleArgValGluGluGlyAsnSerHisAlaGlnTyrValGluAspPro  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCTCCCAGTCATTTGATTCGAGTAGAGGGAAACAGCCATGCCCAGTATGTAGAAGATCCC
Db  805  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  864

Qy  241  IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC
Db  865  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  924

Qy  261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg     280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTGGGGATGAACCGCCGT
Db  925  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  984

Qy  281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACCGTGC
Db  985  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1044

Qy  301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle  320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TTTGAGGCCCGGATCTGCGCTTGCCCAGGAAGAGACAGGAAGGCGGATGAAGAAGATAGCATC
Db 1045  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1104
```

```
Qy  321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT
Db 1105  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1164

Qy  341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAGAGATCCCCAGATGATGAA
Db 1165  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1224

Qy  361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG
Db 1225  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1284

Qy  381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA
Db 1285  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1344

Qy  401  GlnGlnGlnHisGlnHisLeuLeuGlnLysSerAlaCysPheArgAsnGlu           420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CAGCAGCAGCACCAGCACTTACTTCAGAAACATCTCCTTCAGCCTGCTTCAGGAATGAG
Db 1345  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1404

Qy  421  LeuValGlyLeuProArgArgGluThrProLysValProAspPhePheArgHisSerLys  440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGTCTTCTTTAGACATTCCAAG
Db 1405  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1464

Qy  441  ProProAsnArgSerValTyrPro                                       448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCCCCAAACCGATCAGTGTACCCA
Db 1465  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1488

RESULT 3
US-09-850-716A-333
; Sequence 333, Application US/09850716A
; Patent No. US2002011513A1
; GENERAL INFORMATION:
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: McNeill, Patricia D.
;   APPLICANT: Retter, Marc W.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.455C15
;   CURRENT APPLICATION NUMBER: US/09/850,716A
;   CURRENT FILING DATE: 2001-05-07
;   NUMBER OF SEQ ID NOS: 440
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-850-716A-333

Alignment Scores:
Pred. No.:                        Length:        2816
Score:                 1.21e-276  Matches:       448
Percent Similarity:    2383.00    Conservative:  0
Best Local Similarity: 100.00%    Mismatches:    0
Query Match:           100.00%    Indels:        0
DB:                               Gaps:          9

US-09-670-568C-1 (1-448) x US-09-850-716A-333 (1-2816)

Qy    1  MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         ATGTCCCAGAGCACCCAGACCAACGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG
Db  145  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  204

Qy   21  AspPheLeuGluGluCysSerValGlnProIleLeuAspLeuAsnPheValAspGlu     40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GATTTTCTGGAACAGCTATATGTTCAGTTCAGCCCATTGACTTTGTGGATGAA
Db  205  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  264

Qy   41  ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG
Db  265  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  324

Qy   61  AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    441 ProProAsnArgSerValTyrPro 448
          ||||||||||||||||||||||||
Db   1465 CCCCCAAACCGATCAGTGTACCCA 1488
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RESULT 4
US-09-897-778-333
; Sequence 333, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-333

Alignment Scores:
Pred. No.:   1.21e-276   Length: 2816
Score: 2383.00   Matches: 448
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 9

US-09-670-568c-1 (1-448) x US-09-897-778-333 (1-2816)
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Qy     1 MetSerGlnSerThrGlnThrArgAsnGluSerProLeuSerProGlnHisIleTrp 20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204

Qy    21 AspPheLeuGluGlnProIleCysSerValGlnProIleLeuAspLeuAsnPheValAspGlu 40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA 264

Qy    41 ProSerGluAspGlyAlaThrAsnLysIleSerIleGluIleSerMetAspCysIleArgMetGln 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 CCATCAGAAGATGGTGCAACAAACAAGATTAGCATTGAGATTAGCATGGACTGTATCCGCATGCAG 324

Qy    61 AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuLeuAsnSer 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGACCTACACGAACCTGCTCCTGAACAGC 384

Qy    81 MetAspGlnGlnIleGlnAsnGlySerSerSerProTyrArgAsnThrAspHisAla 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCCCATACAGAAACACCGACCACGCG 444

Qy   101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerProPheAspAlaLeu 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGTCCCTTCGATGCTCTC 504

Qy   121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 TCTCCATCACCCGCCATCCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG 564

Qy   141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 TCCTTCCAGCAGTCGAGCACCGCCAAGAGCGCCACCTGGACGTATTCCACTGAACTGAAG 624
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Db   325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACGAACCTGGGCTCCTGAACAGC 384

Qy    81 MetAspGlnGlnIleGlnAsnGlySerSerSerProTyrArgAsnThrAspHisAla 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCCCATACAGAAACACCGACCACGCG 444

Qy   101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerProPheAspAlaLeu 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGTCCCTTCGATGCTCTC 504

Qy   121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 TCTCCATCACCCGCCATCCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG 564

Qy   141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 TCCTTCCAGCAGTCGAGCACCGCCAAGAGCGCCACCTGGACGTATTCCACTGAACTGAAG 624

Qy   161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLeuLysValMetThrProPro 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 AAACTTACTGCCAAATTGCAAGACATGCCCATCCAGATCAAGGTGATGACCCCACCT 684

Qy   181 ProGlnGlyAlaValIleLeuArgAlaMetProValTyrLysAlaGluHisValThrGlu 200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 CCTCAGGGAGCTGTTATCCTGCGGGCCATGCCTGTCTACAAAGCTGAGCACGTCACGGAG 744

Qy   201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleIleAla 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC 804

Qy   221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   805 CCTCCTAGTCATTTGATTCGAGTAGAGGGAAACAGCCATGCCCAGTATGTAGAAGATCCC 864

Qy   241 IleThrGlyArgGlnSerValLeuValProGlnProProGlnValGlyThrGluPhe 260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   865 ATCACAGGAAGACAGAGTGTCTGGTTACCTCAGCCTCCACAGGTTGGCACTGAATTC 924

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCGT 984

Qy   281 ProIleLeuIleGluValThrLeuGluThrArgArgAspGlyValLeuGlyValArgArgCys 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 CCAATTTTAATCATTGTTACCTGGAAACAGAGGAGTGGCAAGTCCTCGGCGCCGACGTGC 1044

Qy   301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgLysAspGluAspSerIle 320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045 TTTGAGGCCCGGATCTGCGCTTGCCCCGGAAGAGACAGGCGGAAGGCCGATGAAGATAGCATC 1104

Qy   321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACAAAGCGCCCGTTTCGT 1164

Qy   341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCTCCAGATGATGAA 1224

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy   381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy   401 GlnGlnGlnHisGlnHisLeuLeuGlnLysGlnThrSerIleGlnSerProSerSerTyrGlyAspLeuMet 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345 CAGCAGCAGCACCAGCACTTACTTCAGAAACAATCTTCTATTCAGTCTCCTTCAGGAATGA 1404

Qy   421 LeuValGluProArgArgGluThrProLysSerAspAspAsnPhePheArgHisSerLys 440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1405 CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGTCTTCTTAGACATTCCAAG 1464
```

APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 333
  LENGTH: 2816
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-007-700-333

Alignment Scores:
Pred. No.:
Score: 1.21e-276   Length: 2816
Percent Similarity: 2383.00   Matches: 448
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 100.00%   Indels: 0
                              14   Gaps: 0

US-09-670-568C-1 (1-448) x US-10-007-700-333 (1-2816)

```
Qy      1  MetSerGlnSerThrGlnThrArgAsnGluPheLeuSerProGluValPheGlnHisIleTrp    20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145  ATGTCCCAGAGCACGCAGACAAGAACAATGAATTCCTCAGTCCAGTGGTTTTCCAGCATATCTGG   204

Qy     21  AspPheLeuGluGlnProIleProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu    40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205  GATTTTCTGGAACAGCCTATATCGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA   264

Qy     41  ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleSerArgMetGln    60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265  CCATCAGAAGATGGTGGCAGCAAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG   324

Qy     61  AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer    80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC   384

Qy     81  MetAspGlnGlnAsnGlySerSerSerProTyrAsnThrAspHisHisAla    100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385  ATGGACCAGCAGAATGGTGGCAGCAAACAAGATTCAGAACGCGTCCTAGCGCCACGCG   444

Qy    101  GlnAsnAsnSerValThrAlaProSerProTyrAlaGlnProHisThrProGluAsnGln    120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445  CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCCAGCTTCCACCTTCGATGCTCTC   504

Qy    121  SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerProPheVal    140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505  TCTCCATCACCCGCCATCCCCTCCAACACGGACTACCCAGGCCCGCACAGTTTCGACGTG   564

Qy    141  SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys    160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565  TCCTTCCAGAGTTCCACTGCGAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG   624

Qy    161  LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro    180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625  AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT   684

Qy    181  ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu    200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685  CCTCAGGGAGCTGTTATCCGCGCCATGCCGGTCTACAAAAAAGCTGAGCACGTCACGGAG   744
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Qy    161  LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro    180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625  AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT   684

Qy    181  ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu    200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685  CCTCAGGGAGCTGTTATCCGCGCCATGCCGGTCTACAAAAAAGCTGAGCACGTCACGGAG   744

Qy    201  ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla    220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745  GTGGTGAAGCGGTGCCCCAACATGAGCTGAGCCGGTGAATTCAACGAGGGACAGATTGCC   804

Qy    221  ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro    240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805  CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC   864

Qy    241  IleThrGlyArgGlnSerValProValLeuValProGlnProGlnValGlyThrGluPhe    260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865  ATCACAGGAAGACAGAGTGTGCCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC   924

Qy    261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg    280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925  ACGACAGTCTTGTACAATTTCATGTGCAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT   984

Qy    281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys    300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    985  CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGGCCGACGCTGC   1044

Qy    301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgAlaAspGluAspSerIle    320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045  TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGACAGGAGGGCCGATGAAGATAGCATC   1104

Qy    321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg    340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1105  AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT   1164

Qy    341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgSerProAspAspGlu    360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165  CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGCCCCGATGACGATGAA   1224

Qy    361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu    380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225  CTGTTATACTTACCCGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG   1284

Qy    381  SerLeuGluLeuMetGlnTyrLeuProHisLysArgThrGluThrTyrArgGlnGlnGln    400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285  TCCCTGGAACTCATGCAGTACCTTCCTCACAAGAGAACAGAAACGTACAGGCAGCAACAA   1344

Qy    401  GlnGlnGlnHisLeuLeuGlnLysSerLeuLeuSerAlaCysPheArgAsnGlu    420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345  CAGCAGCAGCACCAGCACTTACTTCAGAAAACATCTCTTTACTTCAGCCTGCTTCAGGAATGAA   1404

Qy    421  LeuValGluProArgArgGluThrProLysProLysGlnSerPhePheArgHisSerLys    440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1405  CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGTTCTTTAGACATTCCAAG   1464

Qy    441  ProProAsnArgSerValTyrPro    448
           |||||||||||||||||||||||||
Db   1465  CCCCCAAACCGATCAGTGTACCCA   1488
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RESULT 5
US-10-007-700-333
; Sequence 333, Application US200310007700
; Publication No. US20030064947A1
GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.

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; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 333
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-117-982-333

Alignment Scores:
Pred. No.:                                    Length:          2816
Score:                     1.21e-276          Matches:          448
Percent Similarity:        2383.00            Conservative:       0
Best Local Similarity:     100.00%            Mismatches:         0
Query Match:               100.00%            Indels:             0
DB:                        15                 Gaps:               0

US-09-670-568C-1 (1-448) x US-10-117-982-333 (1-2816)
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Qy     1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp  20
Db   145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204

Qy    21 AspPheLeuGluGluProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu  40
Db   205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGACTTTGTGGATGAA 264

Qy    41 ProSerGluAspGlyAlaThrAsnLysIleGluIleLeuSerMetAspCysIleArgMetGln  60
Db   265 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGATGTCATCCGCATGCAG 324

Qy    61 AspSerAspLeuSerAspSerProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer  80
Db   325 GACTCCGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC 384

Qy    81 MetAspGlnIleGlnAsnGlySerSerThrSerProTyrArgAsnThrAspHisAla 100
Db   385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACCAGTCCCTATACACAGAACCACGCG 444

Qy   101 GlnAsnSerValThrArgAlaProSerProTyrArgAlaGlnProSerSerSerThr 120
Db   445 CAGAACAGTGTCACGGCGCCCTCGCCCTACCGCGCACAGTCCTCCAGTTTCGACGTCTC 504

Qy   121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyHisSerPheAspVal 140
Db   505 TCTCCATCACCCGCCATCCCCTCCAACACCGACTACCCGGGCCGCACAGTTTCGACGTG 564

Qy   141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrLysGluLeuLys 160
Db   565 TCCTTCCAGCAGTCGAGCACCGCAGTCGCCACCTGGACGTATTCCACTGAACTGAAG 624

Qy   161 LysLeuTyrCysGlnIleAlaAlaLysThrCysProIleGlnIleLysLysValMetThrProPro 180
Db   625 AAACTCTACTGCCAAATTGCAAATGCAAAGACACATGCCCCATCCAGATCAAGAAGGTGATGACCCCCACCT 684

Qy   181 ProGlnGlyAlaValIleLeuArgAlaMetProValTyrLysValAlaGluHisValThrGlu 200
Db   685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGTCGAGCACGTCACGGAG 744

Qy   201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db   745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGTAGGGAACAGAATTGCC 804

Qy   221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db   805 CCTCCTAGTCATTTGATTCGAGTAGAGGGAACAGCCCAGTATGTAGAAGATCCC 864

Qy   241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db   865 ATCACAGGAAGACAGAGTGTCGTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 924

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db   925 ACGACAGTCTTGTACAATTCATGTGTAACACAGCAGTTGTGTTGGAGGGATGAACCGCGT 984
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Qy   201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db   745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGTAGGGAACAGAATTGCC 804

Qy   221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db   865 ATCACAGGAAGACAGAGTGTCGTGGTACCTTATGAGCCACCCCAGGTGAATTC 924

Qy   241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db   865 ATCACAGGAAGACAGAGTGTCGTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 924

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db   925 ACGACAGTCTTGTACAATTCATGTGTAACACAGCAGTTGTGTTGGAGGGATGAACCCCGT 984

Qy   281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db   985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC 1044

Qy   301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgLysAlaAspGluSerIle 320
Db  1045 TTTGAGGCCCGGATCTGCGCTGCCCCAGGAAGAGACAGGAGGAAGGCCGATGAGAGTATAGCATC 1104

Qy   321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db  1105 AGAAAGCAGCAAGTTTCGACAGTACAAAGAACGGTGATGGTGACGAAGCGGCCGTTTCGT 1164

Qy   341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db  1165 CAGAACACACATGGTATCCAGATGACCATCATCAAGAAACGAAGATCCCCAGATGATGAA 1224

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db  1225 CTGTTATATCTTCCAGTGAGGGGCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy   381 SerLeuGluLeuMetGlnTyrLeuProLysProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db  1285 TCCCTGGAACTCATGCAGTACCTTCCCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy   401 GlnGlnGlnHisGlnHisGluGlnLysTyrLeuGluGlnLysHisLeuLeuLeuSerLeuLeuGlnAsnGln 420
Db  1345 CAGCAGCAGCACCAGCACTTACTTCAGAAAACATCCCTTTCAGCCTGCTTCAGGAATGAG 1404

Qy   421 LeuValGlyLeuProArgGluThrProLysGlnThrProLysLysProAsnGlnAsnSerValProPhePheArgHisSerLys 440
Db  1405 CTTGTGGTGAGCCCCCGGGAGAAGAAACCAAAAACAATCTGACGTCTTCTTAGACATTCCAAG 1464

Qy   441 ProProAsnArgSerValTyrPro 448
Db  1465 CCCCCAAACCGGATCACAGTGTACCCA 1488
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RESULT 6
US-10-117-982-333
; Sequence 333, Application US/10/117982
; Publication No. US20030138438A1
; GENERAL INFORMATION:
;   APPLICANT: Foy, Teresa M.
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Carter, Darrick
;   APPLICANT: Watanabe, Yoshihiro
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Mericle, Barbara
;   APPLICANT: Spies, Gregory A.
;   APPLICANT: Fan, Liqun
;   APPLICANT: Wang, Tongtong
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.455C18
;   CURRENT APPLICATION NUMBER: US/10/117,982
;   CURRENT FILING DATE: 2002-04-05
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Qy    205  GATTTTCGGAACAGCCTATATGTTCAGTCAGCCATTGACTTCAGCCATTGTGGATGAA  264
Db     41  ProSerGluAlaGlyAlaThrAsnLysIleIleSerMetAspCysLysArgMetGln   60
Db    265  CCATCAGAAGATGGTGCACAAACAAGATTGAGATTAGCATGGACTGTAAGCGCATGCAG  324

Qy     61  AspSerAspLeuSerAspProMetTrpProGlnThrThrAsnLeuGlyLeuLeuAsnSer   80
Db    325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGCCTCCTGAACAGC  384

Qy     81  MetAspGlnGlnIleGlnAsnGlyThrSerSerProTyrAsnThrAspHisSerAla    100
Db    385  ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCTATAACACAGACCACCACGCG      444

Qy    101  GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu  120
Db    445  CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCTCCACCTTCGATGCTCTC  504

Qy    121  SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal  140
Db    505  TCTCCATCACCCGCCATCCCTTCCAACACCGACTACCCCGGCCCGCACAGTTTCGACGTG  564

Qy    141  SerPheGlnSerGlnSerThrAlaThrTrpThrTyrSerThrAlaThrTrpThrLeuLys  160
Db    565  TCCTTCCAGTCACGTCGAGCACCGAGCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG  624

Qy    161  LysLeuTyrCysGlnIleIleAlaLysThrCysProIleIleLysLysValMetThrPro  180
Db    625  AAACTCTACTGCCAAATTCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy    181  ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
Db    685  CCTCAGGGAGCTGTTATCCGCGCCATGCCGGTGTACAAAAAAGCTGAGCACGTCACGGAG  744

Qy    201  ValValLysArgCysProAsnHisGluLeuSerArgArgGluGlyPheAsnGlyIleAla  220
Db    745  GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTCGTGAGGGGCACAGAATTGCC    804

Qy    221  ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro  240
Db    805  CCTCCCAGTCATTGATTTGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC  864

Qy    241  IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
Db    865  ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCCCCAGGTTGGCACTGAATTC    924

Qy    261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
Db    925  ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT  984

Qy    281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
Db    985  CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC  1044

Qy    301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgLysGluGluAspSerIle  320
Db   1045  TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGATAGAAGGAAGGAAGAAGATAGCATC  1104

Qy    321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
Db   1105  AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT  1164

Qy    341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
Db   1165  CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA  1224

Qy    361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
Db   1225  CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG  1284

Qy    381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
Db   1285  TCCCTGGAACTGATGCAGTACCTTCCTCAGCACACACAATTGAAACGTTACAGGCAACAA  1344
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Qy    281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
Db    985  CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC  1044

Qy    301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgLysGluGluAspSerIle  320
Db   1045  TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGATAGAAGGAAGGAAGAAGATAGCATC  1104

Qy    321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
Db   1105  AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT  1164

Qy    341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
Db   1165  CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA  1224

Qy    361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
Db   1225  CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG  1284

Qy    381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
Db   1285  TCCCTGGAACTGATGCAGTACCTTCCTCAGCACACACAATTGAAACGTTACAGGCAACAA  1344

Qy    401  GlnGlnGlnHisGlnHisLeuLeuGlnLysGlnThrSerIleGlnSerProSerSerPhe  420
Db   1345  CAGCAGCAGCACCAGCACTTACTTCAGAAACAATCTCCTTCAGCCTCTTCAGGAATGAG    1404

Qy    421  GluAsnLysTyrAlaSerGlnLeuProGlyGlnPheGlnGluSerGlnGluGluSerLys  440
Db   1405  CTTGTGTGAGCCCCGGAGAGAAAACAATCTGACGTCTTCTTTAGACATTCCCAAG      1464

Qy    441  TyrProGlnGlnLysTyrArgSerGlyLeuLysProAsnArgSerValTyrPro      448
Db   1465  CCCCCAAACCGATCAGTGTACCCA                                      1488
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RESULT 7

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US-10-393-590-26
; Sequence 26, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, YIXIN
;  TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
;  FILE REFERENCE: CDS 268 US NP
;  CURRENT APPLICATION NUMBER: US/10/393,590
;  CURRENT FILING DATE: 2003-03-21
;  PRIOR APPLICATION NUMBER: 60/368,789
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 26
;  LENGTH: 2816
;  TYPE: DNA
;  ORGANISM: human
US-10-393-590-26
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Alignment Scores:

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Pred. No.:                                Length:            2816
Score:                   2383.00          Matches:            448
Percent Similarity:      100.00%          Conservative:         0
Best Local Similarity:   100.00%          Mismatches:           0
Query Match:                  16          Indels:               0
DB:                                       Gaps:                 0

                         1.21e-276
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US-09-670-568C-1 (1-448) x US-10-393-590-26 (1-2816)

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Qy      1  MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp  20
Db    145  ATGTCCCAGGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  204

Qy     21  AspPheLeuGlnGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu  40
Db    205  GATTTTCTGCAACAGCCTATATGTTCAGTCCAGCCAATTGAAACGTACAGGCAACAGCAA  1344
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RESULT 8

US-10-393-590-27
; Sequence 27, Application US/10393590
; Publication No. US2003019056A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-27

Alignment Scores:
Pred. No.:   1.21e-276   Length: 2816
Score: 2383.00   Matches: 448
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 16   Gaps: 0

US-09-670-568C-1 (1-448) x US-10-393-590-27 (1-2816)

RESULT 9
US-10-393-590-64
; Sequence 64, Application US/10393590
; Publication No. US2003019056A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789

; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-64

Alignment Scores:
Pred. No.:   1.21e-276
Score: 2383.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 16
DB:

US-09-670-568C-1 (1-448) x US-10-393-590-64 (1-2816)

Qy   1 MetSerGlnThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
Db 145 ATGTCCCAGACAGACACAGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG   204

Qy   21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACAGCCTATATGTTCAGTCCCATTGACTTGAACTTTGTGGATGAA   264

Qy   41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTTCCATGGACTGTATCCGCATGCAG 324

Qy   61 AspSerAspLeuSerAspProMetTrpProGlnThrTyrArgAsnThrAspHisAlaSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGACATACAGAAACACAGACCACGCG   384

Qy   81 MetAspAspGlnIleIleGlnAsnGlySerSerSerThrSerProTyrArgAsnThrAspHisAla 100
Db 385 ATGGACGATCAGATTCAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCG 444

Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerGlnThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGTCCAACCTTCGATGCTCTC 504

Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyHisSerPheAspVal   140
Db 505 TCTCCATCACCCGCCATCCCTTCCAACACCGACTACCCCGGCCACAGCTTCGACGTG   564

Qy 141 SerPheGlnAsnSerSerThrAlaLysSerAlaThrTrpThrTyrThrGluLeuLys   160
Db 565 TCCTTCCAGAACAGTCGACGCCAAGTGCCACCTGGACGATTCCACTGAACTGAAG   624

Qy 161 LysLeuTyrCysGlnIleAlaLysSerProIleGlnIleLeuLysValMetThrProPro 180
Db 625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT 684

Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysValLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG 744

Qy 201 ValValLysSerArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC   804

Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCCAGTCCATTTTGATTCGAGTAGAGGGAAACAGCCATGCCCAGTATGTAGAAGATCCC 864

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 924

Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg   280

Db 925 ACGACAGTCTTGTACAATTCATGTGTACAGAGCAGCAGTTGTGTTGGAGGGATGAACCGCCGT 984

Qy 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAATCATTGTAACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC 1044

Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaGluAspSerIle   320
Db 1045 TTTGAGGCCCGGATCTGTGCTTGCCCCAGGAAGACAGAGGACAGCGAGAAGAGTAGCATC 1104

Qy 321 ArgLysGlnGlnValSerAspSerThrLysAspGlyThrLysAspProPheArg   340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGATGGTACGAAGGACCCCGTTCGT 1164

Qy 341 GlnAsnThrHisGlyIleIleGlnMetThrSerIleLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCAAGAAACGAAGATCCCCAGATGATGAA   1224

Qy 361 LeuLeuTyrLeuProValAlaArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATACTTACCAGTGGAGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACCAATTGAAACGTACAGGCAACAGCAA 1344

Qy 401 GlnGlnHisGlnHisHisLeuLeuGlnLysHisLeuGlnGlnGlnSerAlaProPheArgAsnGlu 420
Db 1345 CAGCAGCAGCACCAGCACTTACTTCAGGAAACATCTCCTTCAGCCTGCTTCAGGAATGAG 1404

Qy 421 LeuValGluProArgArgGluArgLysProLysGlnSerGlnAspValPheArgHisSerLys 440
Db 1405 CTTGTGGAGCCCCGGAGAGAAACGTCCAAAACAATCTGACGTGTCTTTTAGACATTCCAAG 1464

Qy 441 ProProAsnArgSerValTyrPro   448
Db 1465 CCCCCAAACCGATCAGTGTACCCA   1488

RESULT 10
US-10-393-590-65
; Sequence 65, Application US/10393590
; Publication No. US2003019065GA1
; GENERAL INFORMATION:
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
FILE REFERENCE: CDS 268 US NP
CURRENT APPLICATION NUMBER: US/10/393,590
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/368,789
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-65

Alignment Scores:
Pred. No.:   1.21e-276   Length: 2816
Score: 2383.00   Matches: 448
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 16   Indels: 0
DB: Gaps: 0

US-09-670-568C-1 (1-448) x US-10-393-590-65 (1-2816)

Qy   1 MetSerGlnThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
Db 145 ATGTCCCAGACAGACACAGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG   204

Qy   21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40

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Db   1285  TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA  1344

Qy    401  GlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgMetGlu  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345  CAGCAGCAGCACCAGCACCTTACTTCAGAAACATCTCCTTCAGCCTGCTTCAGGAATGAG  1404

Qy    421  LeuValGluProArgArgGluThrProLysGlnSerAspValPheArgHisSerLys  440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1405  CTTGTGGAGCCCCGGAGAGAAACTCCAAAACATCTGAGCGTCTCTTTAGACATTCCAAG  1464

Qy    441  ProProAsnArgValTyrPro  448
           ||||||||||||||||||||
Db   1465  CCCCCAAACCGATCAGTGTACCCA  1488
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RESULT 11
US-10-393-567-26
; Sequence 26, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
;   APPLICANT: WANG, YIXIN
;   TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
;   FILE REFERENCE: CDS 269 US NP
;   CURRENT APPLICATION NUMBER: US/10/393,567
;   CURRENT FILING DATE: 2003-03-21
;   PRIOR APPLICATION NUMBER: 60/368,667
;   PRIOR FILING DATE: 2002-03-29
;   NUMBER OF SEQ ID NOS: 100
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: human
US-10-393-567-26

Alignment Scores:
Pred. No.:   1.21e-276   Length: 2816
Score: 2383.00   Matches: 448
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 16   Indels: 0
DB: Gaps: 0

US-09-670-568C-1 (1-448) x US-10-393-567-26 (1-2816)

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Qy      1  MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisHisTrp  20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145  ATGTCCCAGAGCACAGACACAGAAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  204

Qy     21  AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheAspValAspGlu  40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205  GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  264

Qy     41  ProSerGluAspGlyAlaThrAsnLysIleIleLysSerMetAspCysIleArgMetGln  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265  CCATCAGAAGATGGTGCGACAAACAAGATTAGAGATTGAGACTGTATCCGCATGCAG  324

Qy     61  AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnThrAspHisAlaSer  80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACAACAGAACCTCCTGAACAGC  384

Qy     81  MetAspGlnIleGlnAsnGlySerSerThrSerProTyrAsnThrAspHisAla  100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385  ATGGACCAGCAGATTCAGAACGGCTCTTCCACATACAACACAGACCACGCG  444

Qy    101  GlnAsnThrHisGlyIleGlnMetThrSerIleLysSerArgSerProAspAspGlu  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445  CAGAACAACGTCACGGCGCCCTACCGCCCTACCAGCCCACCACCTTCGATGCTCTC  504

Qy    121  SerProSerProAlaIleProSerAsnArgAspTyrProHisSerPheAspVal  140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505  TCTCCATCACCCGCCATCCCCTCCAACACAGATAACCTCCCCCGACCTG  564

Qy    141  SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerGluLeuLys  160
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; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-27

Alignment Scores:
Pred. No.:             1.21e-276        Length:          2816
Score:                 2383.00          Matches:         448
Percent Similarity:    100.00%          Conservative:    0
Best Local Similarity: 100.00%          Mismatches:      0
Query Match:           100.00%          Indels:          0
DB:                    16               Gaps:            0
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US-09-670-568C-1 (1-448) x US-10-393-567-27 (1-2816)

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Qy     1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  204

Qy    21 AspPheLeuGluGlnProIleCysValSerValGlnProIleLeuAspLeuAsnPheGlu   40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205 GATTTTCTGGAACAGCCTATATGTGTCAGTGTCAGCCCATTTTGACTTGAACTTTGTGGATGAA  264

Qy    41 ProSerGluAspGlyAlaThrAsnLysIleLeuIleSerMetAspCysIleIleArgMetGln   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 CCATCAGAAGATGGTGCGACAAACAAGATTAGAATGAT...                      324

Qy    61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer   80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACAAACCTGGGGCTCCTGAACAGC  384

Qy    81 MetAspGlnGlnIleGlnAsnGlySerSerSerProTyrArgSerThrSerProThrHisAla  100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCCCATATAACAGACCACCGCG         444

Qy   101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrPheAspAlaLeu     120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 CAGAACACAGTGTCACGGGCCCCTGCCCCACGCACAGGTCTCGATGCTGTCTC         504

Qy   121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyHisProHisSerPheAspVal  140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 TCTCCATCACCCGCCATCCCCTCCAACACCGACTACCCAGGCCCCAGTTTCGACGTG     564

Qy   141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerProThrLeuLeuLys   160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565 TCCTTCCAGAGCTCGACCGCCAAGTCGGCCACCTGGACCTATTCCCCTACTGAACTGAAG  624

Qy   161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysLysValMetThrProPro  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGAAGGTGATGACCCCACCT  684

Qy   181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu   200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTGACGGAG  744

Qy   201 ValValLysArgCysProAsnHisGluLeuSerArgGluHisAsnGluGlyGlnIleAla   220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGTCAAGCAGAGTGCC                  804

Qy   221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   805 CCTCCCAGTCATTGATTCGAGTCGAGGGGAACTCCCATGCCCAGTATGTAGAAGATCCC  864

Qy   241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe   260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   865 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  924

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg   280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 ACGACAGTTCTGTACAATTTCATGTGTAACAGTTCCTGTGTGGGAGGCATGAACCGCCGT  984

Qy   281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 CCAATTTTAATCATTGTAACTCTGGAAACCAGAGACGGCCAAGTCCTGGGCCGACGCTGC  1044

Qy   301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle   320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045 TTTGAGGCGCGGATCTGTGCCTGTCCCGGGAGAGACAGGAAGGCGGATGAAGATAGCATC  1104

Qy   321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg   340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGACGGTACGAAGCGCCCGTTTCGT  1164

Qy   341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu   360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165 CAGAACACACATGGTATCCAGATGACTAGCATCAAGAAGAGACGAAGATCCCCAGATGATGAA  1224

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu   380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225 CTGTTATACTTACCAGTGAGGGGTCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG  1284

Qy   381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln   400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA  1344

Qy   401 GlnGlnGlnHisGlnHisLeuLeuLeuGlnLysGlnThrSerIleGlnSerProSerSerTyr  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345 CAGCAGCAGCACCAGCACTTACTTCAGAAACAATCTCCTTCAGCCTCTTCAGGAATGAG  1404

Qy   421 LeuValGluProArgArgGlnThrProLysGlnSerGlnArgPhePheHisArgHisSerLys  440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1405 CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCCCAAAGATTCTTCTTTAGACATTCCAAG  1464

Qy   441 ProProAsnArgSerValTyrPro    448
           ||||||||||||||||||||||||
Db  1465 CCCCCAAACCGATCAGTGTACCCA  1488
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Qy   21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu   40
Db 205 GATTTTCTTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA 264

Qy   41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln   60
Db 265 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG 324

Qy   61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer   80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGCCTCCTGAACAGC 384

Qy   81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCG 444

Qy 101 GlnAsnThrAlaProSerProTyrAlaGlnProSerThrPheAspAlaLeu 120
Db 445 CAGAACACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCTCCACCTTCGATGCTCTC 504

Qy 121 SerProProAlaIleProSerGluAsnThrAspTyrProHisSerPheAspVal 140
Db 505 TCTCCATCACCCGCCATCCCCTCCGAGAATACAGACTACCCGCACAGTTTCGACGTG 564

Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCCAGCAGTCGAGCACCGCCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG 624

Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT 684

Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG 744

Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGTCGAGAGTTCAACGAGGGACAGATTGCC 804

Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC 864

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGACAGCAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 924

Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT 984

Qy 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC 1044

Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTGCTTGCCCAGGTAGAGACAGGAAAGCGGATGAAGACAGCATC 1104

Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAATGGTGATGGCACGAAACGCCCGTTTCGT 1164

Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGTCCTGACGATGAAGAG 1224

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAACTTATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysLeuLeuSerLeuSerAlaCysPheArgAsnGln 420
Db 1345 CAGCAGCAGCAGCACCAGCACTTACTTCAGAAACATCTCCTTTCAGCCTGTTTCAGGAATGAG 1404

Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGTCTTCTTTAGACATTCCAAG 1464

Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAAACCGATCAGTGTACCCA 1488

RESULT 13

US-10-393-567-64
; Sequence 64, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/366,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 64
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-64

Alignment Scores:

Pred. No.:		Length:	2816
Score:	1.21e-276	Matches:	2816
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:		Indels:	0
DB:		Gaps:	0
			16

US-09-670-568C-1 (1-448) x US-10-393-567-64 (1-2816)

Qy   1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
Db 145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204

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Db   1285 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TCCCTGGAACTCCATGCAGTAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy    401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 CAGCAGCAGCACCAGCACTTACTTCAGAAACATCTCCTTCAGCCTGCTTCAGGAATGAG 1404

Qy    421 LeuValGluProArgArgGluThrProLysSerGlnSerPheAspPheArgHisSerLys 440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1405 CTTGTGGAGCCCGGAGAAACTCCAAAACAATCTGACGTCTTCTTTAGACATTCCAAG 1464

Qy    441 ProProAsnArgSerValTyrPro 448
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Db   1465 CCCCCAAACCGATCAGTGTACCCA 1488

RESULT 14
US-10-393-567-65
; Sequence 65, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 65
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-65

Alignment Scores:
Pred. No.:                          Length:       2816
Score:                 2383.00      Matches:      448
Percent Similarity:    100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:   0
Query Match:           100.00%      Indels:       0
DB:                    16           Gaps:         0

                       1.21e-276

US-09-670-568C-1 (1-448) x US-10-393-567-65 (1-2816)

Qy     1 MetSerGlnSerThrGlnHisThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
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Db   145 ATGTCCCAGAGCACCAGACAGATGAATTCCTCAGTCCCAGAGGTTTTCCAGCATATCTGG 204

Qy    21 AspPheLeuGluGluCysSerValGlnProIleAspPheLeuAsnPheValAspGlu 40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205 GATTTTCTGGAAGAGTGTATGTCAGTTCAGCCTATTGACTTTGAACTTTGTGGATGAA 264

Qy    41 ProSerGluAspGlyValAlaThrAsnLysIleGluSerMetAspCysIleArgMetGln 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG 324

Qy    61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC 384

Qy    81 MetAspGlnAsnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385 ATGGACCAGAACATCCAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCG 444

Qy   101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerPheThrPheAspPheAlaLeu 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445 CAGAACAGCGTCACGGCGCCCAGCCCGTACGCCCAGCCCAGCTCCTTCGATGCTCTC 504

Qy   121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505 TCTCCATCACCCGCCATCCCCTCCAACACCGACTACCCCGGCCCCCACAGTTTCGACGTG 564
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Right column:

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Db   141 SerPheGlnSerSerThrAlaLysSerAlaThrThrTyrSerThrGluLeuLys 160
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Qy   565 TCCTTCCAGAGCTCGAGCACCGCCAAGTCGGCCACCACCTACTCCACTGAACTGAAG 624

Qy   161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLeuLysValMetThrProPro 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625 AAACTCTACTGCCAAATTGCAAAGACAATGCCCATCCAGATCCTCAAGGTGATGACCCCACCT 684

Qy   181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG 744

Qy   201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC 804

Qy   221 ProProSerHisLeuIleArgValGluValLysAsnSerHisAlaGlnTyrValGluAspPro 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   805 CCTCCCAGTCATTTGATTCGAGTAGAGGGGAACAGCCCATGCCCAGTATGTGAAGGATCCC 864

Qy   241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   865 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 924

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT 984

Qy   281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC 1044

Qy   301 PheGluGluAlaArgIleCysAlaCysProGlyArgAspArgArgLysAlaAspAspSerIle 320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045 TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGACAGGAGGAAGGCGGATGAAGATAGCATC 1104

Qy   321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysProPheArg 340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105 AGAAAGCAGCAGGTTTCCGACAGTACAAAGAACGGTGATGGTACGAAGCCCGTTTCGT 1164

Qy   341 GlnAsnThrHisGlyIleIleGlnMetThrSerIleLysSerArgArgSerProAspAspGlu 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165 CAGAACACACATGGTATCCAGATGACAAGCATCCATCAAGAGAATCCATCAGAAGATGATGAA 1224

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLeuGlyLys 380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy   381 SerLeuGluLeuMetGlnThrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285 TCCCTGGAACTCATGCAGACTTTGCCACAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy   401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345 CAGCAGCAGCACCAGCACTTACTTCAGAAACATCTCCTTCAGCCTGCTTCAGGAATGAG 1404

Qy   421 LeuValGluProArgArgGluThrProLysSerGlnSerPheAspPheArgHisSerLys 440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1405 CTTGTGGAGCCCGGAGAAACTCCAAAACAATCTGACGTCTTCTTTAGACATTCCAAG 1464

Qy   441 ProProAsnArgSerValTyrPro 448
         ||||||||||||||||||||||||
Db  1465 CCCCCAAACCGATCAGTGTACCCA 1488

RESULT 15
US-10-394-087-26
; Sequence 26, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
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; CURRENT FILING DATE:  2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-394-087-26
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Alignment Scores:
Pred. No.:                      Length:          2816
Score:          1.21e-276       Matches:         448
Percent Similarity: 2383.00     Conservative:    0
Best Local Similarity: 100.00%  Mismatches:      0
Query Match:    100.00%         Indels:          0
Db:             100.00%         Gaps:            16
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US-09-670-568C-1 (1-448) x US-10-394-087-26 (1-2816)

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Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
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Db    145 ATGTCCCAGAGCACCACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  204

Qy     21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu   40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  264

Qy     41 ProSerGluAspGlyAlaThrAsnLysIleSerGluIleSerMetAspCysIleArgMetGln   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 CCATCAGAAGATGGTGCGACAAACAAGATTAGTGAGATTAGCATGGACTGTATCCGCATGCAG  324

Qy     61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer   80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC  384

Qy     81 MetAspGlnIleLeuGlnAsnGlyTyrSerSerSerThrSerProTyrAsnThrAspHisAla  100
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Db    385 ATGGACCAGATTCAGAACGGCTCTCCTCGTCCACAGTCCTATAACACAGACCACGCG  444

Qy    101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrProPheAspAlaLeu  120
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Db    445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGTACACCTTCGATGCTCTC  504

Qy    121 SerProSerProAlaIleProSerArgAsnThrAspTyrProGlyProHisSerPheAspVal  140
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Db    505 TCTCCATCACCCGCATCCCCTCCAACACCGACTACCCCAGGCCCGCACAGTTTGACGTG  564

Qy    141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys  160
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Db    565 TCCTTCCAGCAGTCGAGCACCGCCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG  624

Qy    161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy    181 ProGlnGlyAlaValLeuArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
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Db    685 CCTCAGGGAGCTGTTATCCGCGCCATGCCAGTCTACAAAAAGCTGAGCACGTCACGGAG  744

Qy    201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC  804

Qy    221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTGGAAGATCCC  864

Qy    241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
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Db    865 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  924
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Qy    261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
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Db    925 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT  984

Qy    281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
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Db    985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC  1044

Qy    301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle  320
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Db   1045 TTTGAGGCCCGGATCTGTGCCTGCCCAGGAAGAGACAGGAAGGCGGATGAAGATAGCATC  1104

Qy    321 ArgLysGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
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Db   1105 AGAAAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGGTACGAAGGCCCGTTTCGT  1164

Qy    341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
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Db   1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAAAGAAGATCCCAGATGATGAA  1224

Qy    361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 CTGTTATATCTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG  1284

Qy    381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACCAATTGAAACGTACAGGCAACAGCAA  1344

Qy    401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 CAGCAGCAGCACCAGCACTTACTTCAGAAAACATCTCCTTTCAGCCTGCTTCAGGAATGAG  1404

Qy    421 LeuValGluProLysArgGluLysProLysGlnThrProLysLeuLeuAsnSer  440
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Db   1405 CTTGTGGAGCCCCGGGAGAGAAACTCCAAAACAATCTGACGTCTTCTTTAGACATTCCAAG  1464

Qy    441 ProProAsnArgSerValTyrPro  448
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Db   1465 CCCCCAACCGATCAGTGTACCCA  1488
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Search completed: October 3, 2005, 06:22:31
Job time : 971 secs

OM nucleic - nucleic search, using sw model

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            GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

Run on:     October 3, 2005, 07:53:40 ; Search time 2185 Seconds
                                (without alignments)
                         8898.633 Million cell updates/sec

Title:          US-09-670-568C-2
Perfect score:  2816
Sequence:       2816
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       7442561 seqs, 3452238358 residues

Total number of hits satisfying chosen parameters:    14885122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB	ID	Description
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2	2816	100.0	2816	9	US-09-850-716A-333	Sequence 333, App
3	2816	100.0	2816	9	US-09-897-778-333	Sequence 333, App
4	2816	100.0	2816	14	US-10-007-700-333	Sequence 333, App
5	2816	100.0	2816	15	US-10-117-982-333	Sequence 333, App
6	2816	100.0	2816	16	US-10-393-590-26	Sequence 26, Appl
7	2816	100.0	2816	16	US-10-393-590-27	Sequence 27, Appl
8	2816	100.0	2816	16	US-10-393-590-64	Sequence 64, Appl
9	2816	100.0	2816	16	US-10-393-590-65	Sequence 65, Appl
10	2816	100.0	2816	16	US-10-393-567-26	Sequence 26, Appl
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13	2816	100.0	2816	16	US-10-393-567-65	Sequence 65, Appl
14	2816	100.0	2816	16	US-10-394-087-26	Sequence 26, Appl
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20	2816	100.0	2816	22	US-10-922-124-333	Sequence 333, App
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22	2270	48.9	1376	9	US-09-850-716A-332	Sequence 332, App
23	2270	48.9	1376	9	US-09-897-778-332	Sequence 332, App
24	2270	48.9	1376	14	US-10-007-700-332	Sequence 332, App
25	2270	48.9	1376	15	US-10-117-982-332	Sequence 332, App
26	2270	48.9	1376	17	US-10-313-986-332	Sequence 332, App
27	2270	48.9	1376	20	US-10-775-972-332	Sequence 332, App
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29	4932	48.5	1365	21	US-10-887-553A-596	Sequence 596, App
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31	4849	48.4	1364	9	US-09-850-716A-335	Sequence 335, App
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37	4849	48.4	1364	20	US-10-775-972-335	Sequence 335, App
38	4849	48.4	1364	22	US-10-922-124-335	Sequence 335, App
39	1347	47.8	1347	19	US-10-716-359-3	Sequence 3, Appli
40	1232	43.8	1232	9	US-09-735-705-337	Sequence 337, App
41	1551	43.8	1232	9	US-09-850-716A-337	Sequence 337, App
42	1551	43.8	1232	9	US-09-897-778-337	Sequence 337, App
43	1551	43.8	1232	14	US-10-007-700-337	Sequence 337, App
44	1551	43.8	1232	15	US-10-117-982-337	Sequence 337, App
45	1551	43.8	1232	17	US-10-313-986-337	Sequence 337, App

ALIGNMENTS

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RESULT 1
US-09-735-705-333

; Sequence 333, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT: Fan, Liqun
;  APPLICANT: Kalos, Michael D.
;  APPLICANT: Bangur, Chaitanya S.
;  APPLICANT: Hosken, Nancy
;  APPLICANT: Fanger, Gary R.
;  APPLICANT: Li, Samuel X.
;  APPLICANT: Wang, Aijun
;  APPLICANT: Skeiky, Yasir A.W.
;  APPLICANT: Henderson, Robert A.
;  APPLICANT: McNeill, Patricia D.
;  APPLICANT: Fanger, Neil
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C14
;  CURRENT APPLICATION NUMBER: US/09/735,705
;  CURRENT FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 419
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 333
;  LENGTH: 2816
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-735-705-333
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Query Match          100.0%;  Score 2816;  DB 9;  Length 2816;
Best Local Similarity 100.0%;  Pred. No. 0;  Indels 0;  Gaps 0;
Matches 2816; Conservative 0;  Mismatches 0;

Qy      1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT 60
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Db      1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT 60

Qy     61 ACAGTACTGCCCTGACCCTTACATCGCGTTTCGTAGAAACCCAGCTCATTCTCTTGG 120
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Db     61 ACAGTACTGCCCTGACCCTTACATCGCGTTTCGTAGAAACCCAGCTCATTCTCTTGG 120

Qy    121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAATTCCTCAGT 180
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Db    121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAATTCCTCAGT 180

Qy    181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTCC 240
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Db    181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTCC 240

Qy    241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT 300
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Db    241 ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT 300

Qy    301 AGCATGACTGTATCCGATCAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
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Db    301 AGCATGACTGTATCCGATCAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360

Qy    361 ACGAACCTGGGGCTCCTGACAACAGCAGCAGATTCAGAACGGCTCCTCGTCCACC 420
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Db    361 ACGAACCTGGGGCTCCTGACAACAGCAGCAGATTCAGAACGGCTCCTCGTCCACC 420

Qy    421 AGTCCCTATAACAGACAGACCACGCGCAGAACAGCGTCACGGCCCTCGCCCTACGCACAG 480
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Db    421 AGTCCCTATAACAGACAGACCACGCGCAGAACAGCGTCACGGCCCTCGCCCTACGCACAG 480

Qy    481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGGCCATCCCCTCCAACACCGACTAC 540
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Db    481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGGCCATCCCCTCCAACACCGACTAC 540

Qy    541 CCAGGCCCGCACAGTTCGACGTGTCCTTCCAGCAGTCGGTGAAGCCGTGAGCCTGAGCCGT 600
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Db    541 CCAGGCCCGCACAGTTCGACGTGTCCTTCCAGCAGTCGGTGAAGCCGTGAGCCTGAGCCGT 600

Qy    601 TGGACGTATTCCACTGAACTGAAGAAGAACTCTACTGCCAAATTGCAAAGCACATGCCCCATC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGGACGTATTCCACTGAACTGAAGAAGAACTCTACTGCCAAATTGCAAAGCACATGCCCCATC 660

Qy    661 CAGATCAAGGTGATGACCCCACCTCCTCCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC 720
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Db    661 CAGATCAAGGTGATGACCCCACCTCCTCCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC 720

Qy    721 AAAAAGCTGAGCAGCACGTTGAGCGAGTGGTGAAGCCGTGAGCAACCATGAGCTGAGCCGT 780
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Db    721 AAAAAGCTGAGCAGCACGTTGAGCGAGTGGTGAAGCCGTGAGCAACCATGAGCTGAGCCGT 780

Qy    781 TGTGTTGGAGGGGATGAACCGCCGTCAAATTGATTCGAGTAGAGGGGAACAGC 840
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Db    781 TGAATTCAAGAGGGGACAGATTGCCCCTCCAGTCATTGATTCGAGTAGAGGGGAACAGC 840

Qy    841 CATGCCCCAGTAGTGTGAAGATCCATCACAGGAAGACAGAGTGTTGCTGTGACCTTATGAG 900
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Db    841 CATGCCCCAGTAGTGTGAAGATCCATCACAGGAAGACAGAGTGTTGCTGTGACCTTATGAG 900

Qy    901 CCACCCCAGTTGGCACTGACTTGTACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCACCCCAGTTGGCACTGACTTGTACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy    961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTAATCATTGTACTCTCGGAAACCAGAGAT 1020
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Db    961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTAATCATTGTACTCTCGGAAACCAGAGAT 1020

Qy   1021 GGGCAAGTCCTGGGCCGACGGCTGCTTTGAGGCCCGACATCGTGCTTGCCCAGGACAGAAGAACGGT 1080
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Db   1021 GGGCAAGTCCTGGGCCGACGGCTGCTTTGAGGCCCGACATCGTGCTTGCCCAGGACAGAAGAACGGT 1080

Qy   1081 AGGAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACGACAGAAGAACGGT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGGAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACGACAGAAGACGGT 1140

Qy   1141 GATGGTACGAAGCGCCCGTTTCGTCAGAACACACATGTATCCAGATGACATCCATCAAG 1200
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Db   1141 GATGGTACGAAGCGCCCGTTTCGTCAGAACACACATGTATCCAGATGACATCCATCAAG 1200

Qy   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTCAGTACCTTCCTCAGCACACA 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTCAGTACCTTCCTCAGCACACA 1320

Qy   1321 ATTGAAACGTACAGGCAACAACAGCAGCAGCAACAGCACCACTACTTCAGAAACATCTC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGAAACGTACAGGCAACAACAGCAGCAGCAACAGCACCACTACTTCAGAAACATCTC 1380

Qy   1381 CTTTCAGCCTGCTTCAGGAATGAGTGTTGTGTGACCCCATGTGGCCACAGTAC 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTTCAGCCTGCTTCAGGAATGAGTGTTGTGTGATCCCATGTGGCCACAGTAC 1440

Qy   1441 GACGTCTTCTTTAGACATTCCAAGCCCCAAACGATCAGTGTACCCATCAGAGACCCTATC 1500
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Db   1441 GACGTCTTCTTTAGACATTCCAAGCCCCAAACGATCAGTGTACCCATCAGAGCCCTATC 1500

Qy   1501 TCTATATTTTAAGTGTGTGTGTATCTAGCCCTCATAAACAGACTTGAAGACACTTTGGCTCAGAGA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCTATATTTTAAGTGTGTGTGTATTTCGCAGATTTTCGTATCCTTAGACCGGCCATTGGTGGGTGTA 1560

Qy   1561 TGTGTGTGGCGTGTGTATCTAGCCCTCATAAACAGACTTGAAGACACTTTGGCTCAGAGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGTGTGTGGCGTGTGTATCTAGCCCTCATAAACAGACTTGAAGACACTTTGGCTCAGAGA 1620

Qy   1621 CCCAACTGCTCAAAGGCACACAGTAGTGACAAAGCCACTAGTGAGAATCTTTGAAGGGACTCAAACCT 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCCAACTGCTCAAAGGCACACAGTAGTGACAAAGCCACTAGTGAGAATCTTTGAAGGGACTCAAACCT 1680

Qy   1681 TTACAAGAAAGGATGTTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGGTGGGTGAG 1740
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Db   1681 TTACAAGAAAGGATGTTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGGTGGGTGAG 1740

Qy   1741 GAACCACTGTGTTTGTCTGTGTTTGCTGTGAGCTTCTGGGAGGGACTCAGGTGGG 1800
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Db   1741 GAACCACTGTGTTTGTCTGTGTTTGCTGTGAGCTTCTGGGAGGGACTCAGGTGGG 1800

Qy   1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTCGTCTTCTCGTGTTGTTTTTCTAA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTCGTCTTCTCGTGTTGTTTTTCTAA 1860

Qy   1861 AATTCACAGGGAAGCTTTGAGCAGTCTCAAACTTAAGAGTGTCTTTTTAAGAAAAGGAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AATTCACAGGGAAGCTTTGAGCAGTCTCAAACTTAAGAGTGTCTTTTTAAGAAAAGGAG 1920

Qy   1921 AAAAAGTTGTTATTGTCGTGTCAAGTAAGTTGCATAAGGTGACTAGTCGAGACGTCAGA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AAAAAGTTGTTATTGTCGTGTCAAGTAAGTTGCATAAGGTGACTAGTCGAGACGTCAGA 1980

Qy   1981 CCCTTTTAATGCTCGTGTCATGTAATAATATTGCAAGTAGTAATAATTGCAAGTGTCAAGTG 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CCCTTTTAATGCTCGTCATGTAATAATATTGCAAGTAGTAATAATTGCAAGTGTCAAGTG 2040

Qy   2041 TACTGCTGGGCCAGCGAGGTGATCATCAAAAAGTAATCAACTTTGTGGGTGGGGAGAGTTC 2100
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Db   2041 TACTGCTGGGCCAGCGAGGTGATCATCAAAAAGTAATCAACTTTGTGGGTGGGGAGAGTTC 2100

Qy   2101 TTTGTGAGACTTGCATTATTTGTCCTCCCTCATGTGTGAGGTAGAACATTTCTTAAT 2160
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Db  2101 TTTGTGAGAACTTGCATTATTGTGTCCTCCCCATCGTGTAGGTAGAGACATTCTTAAT 2160

Qy  2161 GCTGTGTACCTGCCTGCCACTGTATGTTGGCATCGTGTTATGCTAAAGTTTTTTCTTGTA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCTGTGTACCTGCCTGCCACTGTATGTTGGCATCGTGTTATGCTAAAGTTTTTTCTTGTA 2220

Qy  2221 CATGAAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTTGGCCCCATAGCAGGTGAA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATGAAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTTGGCCCCATAGCAGGTGAA 2280

Qy  2281 CTCATTTTGTGCTTTTAATAGAAAAGACAAATCCACCCCAGTAATAATTGCCCTTACGTAGT 2340
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Db  2281 CTCATTTTGTGCTTTTAATAGAAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy  2341 TGTTTACCATTATTCAAAGCTCAAAGCTCAAAGAATTGAAGCCCTCTCACAAAATCTGTGATT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGTTTACCATTATTCAAAGCTCAAAGCTCAAAGAATTGAAGCCCTCTCACAAAATCTGTGATT 2400

Qy  2401 AATTTGCTTAATTAGAGAGCTTCTATCCCTCAAGCTACCTACCACCATAAAAACCAGCCATATTA 2460
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Db  2401 AATTTGCTTAATTAGAGAGCTTCTATCCCTCAAGCCTACCTACCACCATAAAAACCAGCCATATTA 2460

Qy  2461 CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTTGAGTAAGTGAAGTGAGATCCAAGC 2520
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Db  2461 CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTTGAGTAAGTGAAGTGAGATCCAAGC 2520

Qy  2521 AGACGTGTTAAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
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Db  2521 AGACGTGTTAAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy  2581 TTCTTTTTTTACTCAAAGTTTAGAAGAATCTCTGTTTCTTTTCCATTTTAAAAACATATT 2640
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Db  2581 TTCTTTTTTTACTCAAAGTTTAGAAGAATCTCTGTTTCTTTTCCATTTTAAAAACATATT 2640

Qy  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCACACCCAGT 2700
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Db  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCACACCCAGT 2700

Qy  2701 CACCAGCACTGTATTTTCTGTCGTCACCAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760
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Db  2701 CACCAGCACTGTATTTTCTGTCGTCACCAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760

Qy  2761 TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA 2816
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Db  2761 TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA 2816
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Db    1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT

Qy   61 ACAGTACTGCCCTGACCCTTACATCCACCATCCAGGCGTTCGTGTAGAAACCCAGAGATT 120
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Db   61 ACAGTACTGCCCTGACCCTTACATCCACCATCCAGGCGTTCGTGTAGAAACCCAGAGATT 120

Qy  121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACACAGACAAATGAATTCCTCAGT 180
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Db  121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACACAGACAAATGAATTCCTCAGT 180

Qy  181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTCAGTTCAGTCGCCC 240
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Db  181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGTCGCCC 240

Qy  241 ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAGATGGTGCAAACAGAGATTGAGATT 300
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Db  241 ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAGATGGTGCAAACAGAGATTGAGATT 300

Qy  301 AGCATGACTGTATCCGCATGCAGACTCGGACCTCGGAGTGGCCACAGTAC 360
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Db  301 AGCATGACTGTATCCGCATGCAGACTCGGACCTCGGAGTGGCCACAGTAC 360

Qy  361 ACGAACCTGGGGCTCTGAACAGCATGCAGACCAGATTCAGAACGGCGCCTCCTCCGTCCACC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ACGAACCTGGGGCTCTGAACAGCATGCAGACCAGATTCAGAACGGCGCCTCCTCCGTCCACC 420

Qy  421 AGTCCCTATAACACAGACACCGCGCCGAGAACACAGCGGCTCACGGCGCCTCGCCCTACGCACAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AGTCCCTATAACACAGACACCGCGCCGAGAACACAGCGGCTCACGGCGCCTCGCCCTACGCACAG 480

Qy  481 CCCAGCTTCCACCTTCGATGTCTTCTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC 540
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Db  481 CCCAGCTTCCACCTTCGATGTCTTCTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC 540

Qy  541 CCAGGCCCGCCACAGTTTCGACGTGTCCTCCAGCAGCCGCCAAGTGCCGCCACC 600
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Db  541 CCAGGCCCGCCACAGTTTCGACGTGTCCTCCAGCAGCCGCCAAGTGCCGCCACC 600

Qy  601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC 660
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Db  601 TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC 660

Qy  661 CAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTGTGTATCCGCGCCATGCCTGTCTAC 720
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Db  661 CAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTGTGTATCCGCGCCATGCCTGTCTAC 720

Qy  721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCTCCCCAACCATGAGCTGAGCCGT 780
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Db  721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCTCCCCAACCATGAGCTGAGCCGT 780

Qy  781 GAATTCAACGAGGGACAGAGATTGCCCTCCAGTCATTGATTCGAGTAGAGGGAACAGC 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GAATTCAACGAGGGACAGAGATTGCCCTCCAGTCATTTGATTCGAGTAGAGGGAACAGC 840

Qy  841 CATGCCCAGTATGTGAAAGATCCATCACAGGAAGACAGAGTGTGCTGTGGTACCTTATGAG 900
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Db  841 CATGCCCAGTATGTGAAAGATCCATCACAGGAAGACAGAGTGTGCTGTGGTACCTTATGAG 900

Qy  901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTAATCATTGTTACTCTGGAAACCAGAGAT 960
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Db  901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTAATCATTGTTACTCTGGAAACCAGAGAT 960

Qy  961 TGTGTTGGAGGGATGAACCGCCGACGCGTGCTCTTGAGCCCGGAAGCAGAGAT 1020
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Db 1021 GGCAAGTCCTGGGCCGACGCGTGCTCTTGAGGCCCGGAGATCCCAGGAAGAGAC 1080

Qy 1081 AGGAAGGCGGATGAAGATAGCATCAGAAGCAGCAAGTTTCGGACAGCAGTACAAAGAACGT 1140
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Query Match             100.0%;  Score 2816;  DB 9;  Length 2816;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  2816;  Mismatches    0;  Conservative    0;  Indels    0;  Gaps    0;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GATGGTACGAAGCGCCGTTCGTCAGAACACAACAGGTATCCAGATGACATCCATCAAG 1200

Qy  1201 AAACGAAGAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AAACGAAGAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT 1260

Qy  1261 GAAATGCTGTTGAAGATCAAAGAGTCCTGGAACTCATGCAGTACCTTCCTCAGCACACA 1320
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Db  1261 GAAATGCTGTTGAAGATCAAAGAGTCCTGGAACTCATGCAGTACCTTCCTCAGCACACA 1320

Qy  1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACATCTC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACATCTC 1380

Qy  1381 CTTTCAGCCTGCTTCAGGAATGAGCTGTGGAGCCCCGAGAGAAACTCCAAAACAATCT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTTTCAGCCTGCTTCAGGAATGAGCTGTGGAGCCCCGAGAGAAACTCCAAAACAATCT 1440

Qy  1441 GACGTCTTCTTTAGACATTCCAAGCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GACGTCTTCTTTAGACATTCCAAGCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500

Qy  1501 TCTATATTTTAAGTGTGTGTGTATTCCATGTGTATGTGAGTGTGTGTGTGTGTGTGTA 1560
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Db  1501 TCTATATTTTAAGTGTGTGTGTATTCCATGTGTATGTGAGTGTGTGTGTGTGTGTGTA 1560

Qy  1561 TGTGTGTGGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TGTGTGTGGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620

Qy  1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT 1680

Qy  1681 TTACAAGAAAGGATGTTTCTGCAGATTTCTGCAGATTTTGTATCCTTAGACCGCCATTGGTGGTGAG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TTACAAGAAAGGATGTTTCTGCAGATTTCTGCAGATTTTGTATCCTTAGACCGCCATTGGTGGTGAG 1740

Qy  1741 GAACCACTGTGTTGTCTGTGAGCTTCTGTGTTCCTGGGAGGGGGAGGGGTCAGTGGG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GAACCACTGTGTTGTCTGTGAGCTTCTGTGTTCCTGGGAGGGGGAGGGGTCAGTGGG 1800

Qy  1801 GAAAGGGGCATTAAGACATGTTTATTGGAACCCTTTTCTGTCTCTTCGTTGTTTTTCTAA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GAAAGGGGCATTAAGACATGTTTATTGGAACCCTTTTCTGTCTCTTCGTTGTTTTTCTAA 1860

Qy  1861 AATTCACAGGGAAGCTTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG 1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AATTCACAGGGAAGCTTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG 1920

Qy  1921 AAAAAAGTTGTTATTTGTCTGTCGATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 AAAAAAGTTGTTATTTGTCTGTCGATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA 1980

Qy  1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAAGAAACGAAGGTGTCAAGTG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAAGAAACGAAGGTGTCAAGTG 2040

Qy  2041 TACTGCTGGGCAGCGAGGTGATCATTGTCAAACTTGTGGGTGGAGAGTTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TACTGCTGGGCAGCGAGGTGATCATTGTCAAACTTGTGGGTGGAGAGTTC 2100

Qy  2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCTCCCCTCATGTGTAGGTAGAACATTCTTAAT 2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCTCCCCTCATGTGTAGGTAGAACATTCTTAAT 2160

Qy  2161 GCTGTGTACCTGCCTCGCCACTGTCATCTGTATGCTAAAGTTTTTCTTGTA 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCTGTGTACCTGCCTCGCCACTGTCATCTGTATGCTAAAGTTTTTCTTGTA 2220

Qy  2221 CATGAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCATAGCAGGTGAA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATGAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCATAGCAGGTGAA 2280

Qy  2281 CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy  2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTGAAGCCCTCTCACAAAATCTGTGATT 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTGAAGCCCTCTCACAAAATCTGTGATT 2400

Qy  2401 AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCCTACCTACCATAAAACCAGCCATATTA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCCTACCTACCATAAAACCAGCCATATTA 2460

Qy  2461 CTGATACTGTTCAGTGCATTTGAGTAAGTGTTTGAGTAAGTGAGATCCAAGC 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTGATACTGTTCAGTGCATTTGAGTAAGTGTTTGAGTAAGTGAGATCCAAGC 2520

Qy  2521 AGACGTGTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AGACGTGTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy  2581 TTCTTTTTTTTACTCAAAGTTAGAGAATCTCTGTTCTTCTTCCATTTAAAAACATATT 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TTCTTTTTTTTACTCAAAGTTAGAGAATCTCTGTTCTTCTTCCATTTAAAAACATATT 2640

Qy  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCATCCTTCCCACACCCCAGT 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCATCCTTCCCACACCCCAGT 2700

Qy  2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760

Qy  2761 TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA 2816
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA 2816
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RESULT 3
US-09-897-778-333
; Sequence 333, Application US/09897778
; Patent No. US2002014714A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-333

Query Match   100.0%; Score 2816; DB 9; Length 2816;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  TCGTTGATATCAAAGACAGTTGAAGGAAATGATTTGAAACTTCACGGTGTGCCACCCT  60
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Db      1  TCGTTGATATCAAAGACAGTTGAAGGAAATGATTTGAAACTTCACGGTGTGCCACCCT  60

Qy     61  ACAGTACTGCCCTGACCCTTACATCCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ACAGTACTGCCCTGACCCTTACATCCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120

Qy    121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGACACAGACAAATGAATTCCTCAGT  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGACACAGACAAATGAATTCCTCAGT  180

Qy    181  CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240

Qy    241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300

Qy    301  AGCATGACTGTATCCCGATGCAGGACTCGGACTCGAGTGACCCATGTGGCCACAGTAC  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AGCATGACTGTATCCCGATGCAGGACTCGGACTCGAGTGACCCATGTGGCCACAGTAC  360

Qy    361  ACGAACCTGGGGCTCCTGAACAGCATGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420
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Db    361  ACGAACCTGGGGCTCCTGAACAGCATGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420

Qy    421  AGTCCCTATAACACAGACCACCGCGCAGAACAGCTCACGGGCCCTCGCCCTACGCACAG  480
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Db    421  AGTCCCTATAACACAGACCACCGCGCAGAACAGCTCACGGGCCCTCGCCCTACGCACAG  480

Qy    481  CCCAGTCCACCTTGCATGCTCTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCCAGTCCACCTTGCATGCTCTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC  540

Qy    541  CCAGGCCCGCACAGTTCGACGTGTCCTTCCAGCAGTCGAGCACCGCCAGTCGGCCACC  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCAGGCCCGCACAGTTCGACGTGTCCTTCCAGCAGTCGAGCACCGCCAGTCGGCCACC  600

Qy    601  TGGACGTATTCCACTGACTGAAGAAAACTCTACTGCCAAATTGCAAAGACACATGCCCCATC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TGGACGTATTCCACTGACTGAAGAAAACTCTACTGCCAAATTGCAAAGACACATGCCCCATC  660

Qy    661  CAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTTGTTATCCGCGCCCATGCCTGTCTAC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTTGTTATCCGCGCCCATGCCTGTCTAC  720

Qy    721  AAAAAAGCTGAGCACGTCACGGAGGTGGTCAAGCGGTGAGCCAACCATGAGCTGAGCCGGT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AAAAAAGCTGAGCACGTCACGGAGGTGGTCAAGCGGTGAGCCAACCATGAGCTGAGCCGGT  780

Qy    781  GAATTCAACGAGGGGACAGATGCCCCTCAGTCATTTGATTCGAGTGAGGGGGAACAGC  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GAATTCAACGAGGGGACAGATGCCCCTCAGTCATTTGATTCGAGTGAGGGGGAACAGC  840

Qy    841  CATGCCCAGTATGTAGAAGATCCCATCACAGAAGACAGAGAGTGTGCGTGGTACCTTATGAG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CATGCCCAGTATGTAGAAGATCCCATCACAGAAGACAGAGAGTGTGCGTGGTACCTTATGAG  900

Qy    901  CCACCCCAGGTTGGACTGAATTCACGACAGTCTTGTACAAATTTCATGTGTAACACGCAGT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CCACCCCAGGTTGGACTGAATTCACGACAGTCTTGTACAAATTTCATGTGTAACACGCAGT  960

Qy    961  TGTGTTGGAGGGATGAACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TGTGTTGGGGGGATGAACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT  1020

Qy   1021  GGGCAAGTCCTGGGCCGGATCGTGCTTGCCCAGGCCCGGAGGGAAGAGAC  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGGCAAGTCCTGGGCCGGATCGTGCTTGCCCAGGCCCGGAGGGAAGAGAC  1080

Qy   1081  AGGAAGGGCGGATGAAGATAGCATCAGAAGACAGCAGCAAGTTTCGGACAGTACAAAGAGAACGGT  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1081  AGGAAGGGCGGATGAAGATAGCATCAGAAGACAGCAGCAAGTTTCGGACAGTACAAAGAGAACGGT  1140

Qy   1141  GATGGTACGAAGCGCCCGTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GATGGTACGAAGCGCCCGTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG  1200

Qy   1201  AAACGAAGATCCCAGATGATGAACTGTATACTTACCAGTGAGGGCCGTGAGACTTAT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AAACGAAGATCCCAGATGATGAACTGTATATCTTACCAGTGAGGGCCGTGAGACTTAT  1260

Qy   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA  1320

Qy   1321  ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACATCTC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACATCTC  1380

Qy   1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440

Qy   1441  GACGTCTTCTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GACGTCTTCTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500

Qy   1501  TCTATATTTTAAGTGTGTGTGTATTCATGTGTATATGTGAGTGTGTGTGTGTA  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  TCTATATTTTAAGTGTGTGTGTATTCATGTGTATATGTGAGTGTGTGTGTGTA  1560

Qy   1561  TGTGTGTGCGTGTATCTGAGTTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TGTGTGTGCGTGTATCTGAGTTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620

Qy   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGGACTCAAACCT  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGGACTCAAACCT  1680

Qy   1681  TTACAAGAAAGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TTACAAGAAAGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy   1741  GAACCACTGTGTTGTCTGTGAGCTTCTGTGTTCCTGGGAGGAGGGGTCAGGTGGG  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAACCACTGTGTTGTCTGTGAGCTTCTGTGTTCCTGGGAGGAGGGGTCAGGTGGG  1800

Qy   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTGTTTTCTGTCTGTTTTCTAA  1860
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Db   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTGTTTTCTGTCTGTTTTCTAA  1860

Qy   1861  AATTCACAGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  AATTCACAGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG  1920

Qy   1921  AAAAAAGTTGTATTGTCGTGCATAAGTAAGTTGTGACTGAGGACTCAGTCAGA  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  AAAAAAGTTGTATTGTCGTGCATAAGTAAGTTGTGACTGAGGACTCAGTCAGA  1980

Qy   1981  CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGAGGTGTCAAGTG  2040
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Db   1981  CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGAGGTGTCAAGTG  2040

Qy   2041  TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGTTC  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TACTGCTGGGCAGCGAGGTGATCATTATTTGTCTCCCCCCATGTGTAGGTAGAACATTTCTTAAT  2100

Qy   2101  TTTGTGAGAACTTGCATTATTTGTCTCCCCCCATGTGTAGGTAGAACATTTCTTAAT  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TTTGTGAGAACTTGCATTATTTGTCTCCCCCCATGTGTAGGTAGAACATTTCTTAAT  2160

Qy   2161  GCTGTGTACCTTGCCTCTGCCACTGTTGCCACCTGTTGTATGCTAAAGTTTTTCTTGTA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-007-700-333

Query Match          100.0%;  Score 2816;  DB 14;  Length 2816;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2816;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT   60

Qy    61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTGAGAACCCAGTCATTTCTTCTTGG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTGAGAACCCAGTCATTTCTTCTTGG  120

Qy   121 AAAGAAAGTATTACCGATCCACCATGTCCCAGAGGACACAGACAAATGAATTCCTCAGT  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAGAAAGTATTACCGATCCACCATGTCCCAGAGGACACAGACAAATGAATTCCTCAGT  180

Qy   181 CCGAGGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCGAGGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCC  240

Qy   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAGAGTGGTGCGACAAACAAGATTGAGATT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTGACTTGAACTTTGTGGATGAACCATCAGAGAGTGGTGCGACAAACAAGATTGAGATT  300

Qy   301 AGCATGGACTGTATCCGCATGCAGGACTCGAGTGACCCCATGTGGCCACAGTAC  360
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Db   301 AGCATGGACTGTATCCGCATGCAGGACTCGAGTGACCCCATGTGGCCACAGTAC  360

Qy   361 ACGAACCTGGGGCTCCTGACACAGATTCAGAACGGCTCCTCCGTCCACC  420
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Qy   421 AGTCCCTATAACACAGACCACACGCGCAGAACAGCGTCACGGCGCCCTCGCCACGCACAG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGTCCCTATAACACAGACCACACGCGCAGAACAGCGTCACGGCGCCCTCGCCACGCACAG  480

Qy   481 CCCAGTCCACCTTCGATGCTCTCTCTCCCATCACCCGCCATCCCTCCAACACCACGACTAC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCAGTCCACCTTCGATGCTCTCTCTCCCATCACCCGCCATCCCTCCAACACCACGACTAC  540

Qy   541 CCAGGCCCGCCACAGTTCGACGTGTCTTCCTTCCAGCAGTCGAGCGCCCAAGTCGGCGCCACC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCAGGCCCGCCACAGTTCGACGTGTCTTCCTTCCAGCAGTCGAGCGCCCAAGTCGGCGCCACC  600

Qy   601 TGGAGTATTCCACTGAACTGAAGAAAACTTCTACTGCCAAATTGCAAAGACATGCCCCATC  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGAGTATTCCACTGAACTGAAGAAAACTTCTACTGCCAAATTGCAAAGACATGCCCCATC  660

Qy   661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGGCGGCCATGCCTGTCTAC  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGGCGGCCATGCCTGTCTAC  720

Qy   721 AAAAAGCTGAGCACGTCACGGAGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGGT  780
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Db   721 AAAAAGCTGAGCACGTCACGGAGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGGT  780

Qy   781 GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTTCATTTGATTCGAGTAGAGGGGAACAGC  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTTCATTTGATTCGAGTAGAGGGGAACAGC  840

Qy   841 CATGCCCAGTATGTAGAAGATCCCATCACACAGGAAGAACAGAGTGTCGTGGTACCTTATGAG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CATGCCCAGTATGTAGAAGATCCCATCACACAGGAAGAACAGAGTGTCGTGGTACCTTATGAG  900

Qy   901 CCACCCCAGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
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Db   901 CCACCCCAGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
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Db  2161 GCTGTGTACCTCGCCTGCCACTGTATGTTGGCATCTGTTGTATGCTAAAGTTTTCTTGTA  2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 CATGAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA   2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATGAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA   2280

Qy  2281 CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340
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Db  2281 CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340

Qy  2341 TGTTTACCATTATTCAAAGCTCAAAAGTCAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGTTTACCATTATTCAAAGCTCAAAAGTCAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400

Qy  2401 AATTTGCTTAATTAGAGCTTCTATCCCTCAGCCTACCTACCATAAAACCAGCCATATTA  2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AATTTGCTTAATTAGAGCTTCTATCCCTCAGCCTACCTACCATAAAACCAGCCATATTA  2460

Qy  2461 CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC  2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC  2520

Qy  2521 AGACGTGTTAAAATCAGCACTCCTGGACTTGGAAATTAAAGATTGAAAGGGTAGACTACTT  2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AGACGTGTTAAAATCAGCACTCCTGGACTTGGAAATTAAAGATTGAAAGGGTAGACTACTT  2580

Qy  2581 TTCTTTTTTTTACTTCAAAAGTTTAGAGAATCTCTGTTCTTCCTCCCCCCATCTTCCCACACCAGT  2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TTCTTTTTTTTACTTCAAAAGTTTAGAGAATCTCTGTTCTTCCTCCCCCCATCTTCCCACACCAGT  2640

Qy  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCCATCTTCCCCACACCCCAGT  2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCCATCTTCCCCACACCCCAGT  2700

Qy  2701 CACCAGCACTGTATTTTCTGTCACCAAGACAAATGAGATTTCTTGTTATTGAGGCTGTTGCTT  2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CACCAGCACTGTATTTTCTGTCACCAAGACAAATGAGATTTCTTGTTATTGAGGCTGTTGCTT  2760

Qy  2761 TTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTGTTTAAAGAAA  2816
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Db  2761 TTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTGTTTAAAGAAA  2816
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RESULT 4
US-10-007-700-333
;   Sequence 333, Application US/10007700
;   Publication No. US20030064947A1
GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Li, Samual X.
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: McNeill, Patricia D.
;   APPLICANT: Fanger, Neil
;   APPLICANT: Retter, Marc W.
;   APPLICANT: Durham, Margarita
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Vedvick, Thomas S.
;   APPLICANT: Carter, Darrick
;   APPLICANT: Watanabe, Yoshihiro
;   APPLICANT: Peckman, David W.
;   APPLICANT: Cai, Feng
;   APPLICANT: Foy, Teresa M.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.455C17
;   CURRENT APPLICATION NUMBER: US/10/007,700
;   CURRENT FILING DATE: 2001-11-30
;   NUMBER OF SEQ ID NOS: 469
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 333
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Qy    961  TGTGTTGGAGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TGTGTTGGAGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT  1020

Qy   1021  GGGCAGTCCTGGCCGACGCTGCTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGAC  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGGCAGTCCTGGCCGACGCTGCTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGAC  1080

Qy   1081  AGGAAGGCGGATGAAGATAGCAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGT  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  AGGAAGGCGGATGAAGATAGCAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGT  1140

Qy   1141  GATGGTACGAAGCGCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GATGGTACGAAGCGCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG  1200

Qy   1201  AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT  1260

Qy   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCAGTACCTTCCTCAGCACACA  1320

Qy   1321  ATTGAAAACGTACAGGCAACAGCAGCAGCACCAGCACTTACTTCAGAAAACATCTC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATTGAAAACGTACAGGCAACAGCAGCAGCACCAGCACTTACTTCAGAAAACATCTC  1380

Qy   1381  CTTTCAGCCTGCTTCTTAGACATTGAGCTTGTGTGGAGCCCCCAAGGAGAGAAACTCCAAAACAATCT  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTTTCAGCCTGCTTCTTAGACATTGAGCTTGTGTGGAGCCCCCAAGGAGAGAAACTCCAAAACAATCT  1440

Qy   1441  GACGTCTCTTCTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCGAATCAGCCCCTATC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GACGTCTCTTCTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCGAATCAGCCCCTATC  1500

Qy   1501  TCTATATTTAAGTGTGTGTGTATTTCCATGTGTATGTGAGTGTGTGTGTGTA  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  TCTATATTTAAGTGTGTGTGTATTTCCATGTGTATGTGAGTGTGTGTGTGTA  1560

Qy   1561  TGTGTGGCGTGTGTATCCCTCATAAAACAGGACTTGAAGACACACTTTGGCTCAGAGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TGTGTGGCGTGTGTATCCCTCATAAAACAGGACTTGAAGACACACTTTGGCTCAGAGA  1620

Qy   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAATCTTTGAAGGGACTCAAACCT  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAATCTTTGAAGGGACTCAAACCT  1680

Qy   1681  TTACAGAAAGGATGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TTACAGAAAGGATGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy   1741  GAACCACTGGTCGTGTTGTCTGTGAGCTTTCTGTGTTCTTCGTGTTCTTCGTGTTTCTAA  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAACCACTGGTCGTGTTGTCTGTGAGCTTTCTGTGTTCTTCGTGTTCTTCGTGTTTCTAA  1800

Qy   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCCTTTCGTCTTTCGTGTTTCGTGTTTCTAA  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCCTTTCGTCTTTCGTGTTTCGTGTTTCTAA  1860

Qy   1861  AATTCACAGGGAAGCTTTTGACGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  AATTCACAGGGAAGCTTTTGACGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920

Qy   1921  AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA  1980

Qy   1981  CCCTTTTAATCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGGTGTCAAGTG  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CCCTTTTAATCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGGTGTCAAGTG  2040

Qy   2041  TACTGCTGGGCAGCGAGTGATGATCATTACCACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TACTGCTGGGCAGCGAGTGATGATCATTACCACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC  2100

Qy   2101  TTTGTGAGAACTTGCATTATTTGTCCTCCCCTCCCCCATGTGTAGGTAGAACATTTCTTAAT  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TTTGTGAGAACTTGCATTATTTGTCCTCCCCTCCCCCATGTGTAGGTAGAACATTTCTTAAT  2160

Qy   2161  GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTTATCGTAAAGTTTTTCTTGTA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTTATCGTAAAGTTTTTCTTGTA  2220

Qy   2221  CATGAAACCCTGGAAGACCTACTACAAAAAAAACTGTTGTTTGGCCCCATAGCAGGTGAA  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CATGAAACCCTGGAAGACCTACTACAAAAAAAACTGTTGTTTGGCCCCATAGCAGGTGAA  2280

Qy   2281  CTCATTTTGTGCTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTCATTTTGTGCTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340

Qy   2341  TGTTTACCATTATTCAAAGCTCAAAATAGAATTGAAGCCCTCTCACAAAATCTGTGATT  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  TGTTTACCATTATTCAAAGCTCAAAATAGAATTGAAGCCCTCTCACAAAATCTGTGATT  2400

Qy   2401  AATTTGCTTAATTAGAGCTTCTATCCCTCCAAGCCTCACCATTAAAACCAGCCATATTA  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  AATTTGCTTAATTAGAGCTTCTATCCCTCCAAGCCTCACCATTAAAACCAGCCATATTA  2460

Qy   2461  CTGATACTGTTCAGTGCATTAGCACGGAGACTACGTTTGAGTAAGTGAGATCCAAGC  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTGATACTGTTCAGTGCATTAGCACGGAGACTACGTTTGAGTAAGTGAGATCCAAGC  2520

Qy   2521  AGACGTGTTAAAAATCAGCACTCCTGGAAATTAAAGATTGAAAAGGTAGACTACTT  2580
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Db   2521  AGACGTGTTAAAAATCAGCACTCCTGGAAATTAAAGATTGAAAAGGTAGACTACTT  2580

Qy   2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTCCATTTTAAAAACATATT  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTCCATTTTAAAAACATATT  2640

Qy   2641  TTAAGATAATAGCATAAAGACTTAAAAATGTTCCCCGCCCCATCTTCCCACACCCAGT  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  TTAAGATAATAGCATAAAGACTTAAAAATGTTCCCCGCCCCATCTTCCCACACCCAGT  2700

Qy   2701  CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTGTTATTGAGGCTGTTGCTT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTGTTATTGAGGCTGTTGCTT  2760

Qy   2761  TTGTGGATGTGTGATTTTAATTTCAATAAAACTTTCAATCTTTGCATCTTTGGTTTTAAAAGAAA  2816
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Db   2761  TTGTGGATGTGTGATTTTAATTTCAATAAAACTTTCAATCTTTGCATCTTTGGTTTTAAAAGAAA  2816
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; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 333
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-117-982-333

Query Match             100.0%;
Best Local Similarity   100.0%;
Matches 2816;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

SEQ ID NOS: 484
Score 2816;   DB 15;   Length 2816;
Pred. No. 0;
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Qy      1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTCTGCCACCCT    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTCTGCCACCCT    60

Qy     61  ACAGTACTGCCCTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG       120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ACAGTACTGCCCTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG       120

Qy    121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT   180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT   180

Qy    181  CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240

Qy    241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300

Qy    301  AGCATGGACTGTATCCGACTCGGAGGACTCCATGTGACCTGAGTTGCCCACTACGGCACAC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AGCATGGACTGTATCCGACTCGGAGGACTCCATGTGACCTGAGTTGCCCACTACGGCACAC 360

Qy    361  ACGAACCTGGGGCTCCTGAACAGCAGCAGATTCAGAACGGCTCCTCGTCCACC         420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  ACGAACCTGGGGCTCCTGAACAGCAGCAGATTCAGAACGGCTCCTCGTCCACC         420

Qy    421  AGTCCCTATAACACAGACCACGGCGAGAACAGCGTCACGGCCCCTCGCCGGCCTACGGCACAG 480
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Db    421  AGTCCCTATAACACAGACCACGGCGAGAACAGCGTCACGGCCCCTCGCCGGCCTACGGCACAG 480

Qy    481  CCCAGCTCCACCTTCGATGCTGTCTCTCCCATCACCCCGCCATCCCCCACACACCGACTAC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  CCCAGCTCCACCTTCGATGCTGTCTCTCCCATCACCCCGCCATCCCCCACACACCGACTAC  540

Qy    541  CCAGGCCCGCACAGTTCGACGTGTCTTCCAGCTGTCCTTCCAGCAGTCAGTTGGCCACC    600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCAGGCCCGCACAGTTCGACGTGTCTTCCAGCTGTCCTTCCAGCAGTCAGTTGGCCACC    600

Qy    601  CAGATCAAGGTGATGACGCCACCCTCCAGGGAGCGTGTTATCCGCAAATGCAAAAGACATGCCCCATC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CAGATCAAGGTGATGACGCCACCCTCCAGGGAGCGTGTTATCCGCAAATGCAAAAGACATGCCCCATC 660

Qy    661  TGGACGTATTCCACTGAACTGAAGAAACTTACTGCCAAGGGCCATGCCGCCATGGCCTCTAC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  TGGACGTATTCCACTGAACTGAAGAAACTTACTGCCAAGGGCCATGCCGCCATGGCCTCTAC 720

Qy    721  AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCCGGTGCCCCAACCATGAGCTGAGCCGT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCCGGTGCCCCAACCATGAGCTGAGCCGT  780

Qy    781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGC  840

Qy    841  CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGCACAGAGTGTGCTGGTACCTTATGAG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGCACAGAGTGTGCTGGTACCTTATGAG  900

Qy    901  CCACCCCAGGTTGGCACTGGCACTGGAATTCACGACAGTCTTGTACAATTCATGTGTAACAGCAGT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CCACCCCAGGTTGGCACTGGCACTGGAATTCACGACAGTCTTGTACAATTCATGTGTAACAGCAGT 960

Qy    961  TGTGTTGGAGGGATGAACCGGCGCACGCCGTCCAATTTAATCATTGTACTCTGGAAACCAGAGAT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TGTGTTGGAGGGATGAACCGGCGCACGCCGTCCAATTTAATCATTGTACTCTGGAAACCAGAGAT 1020

Qy   1021  GGGCAAGTCTGGCCGACGCTGCTTTGAGCGCCGACATCGTGCTGCCCAGAAGAGAC    1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGGCAAGTCTGGCCGACGCTGCTTTGAGCGCCGACATCGTGCTGCCCAGAAGAGAC    1080

Qy   1081  AGGAAGGCGGATGAAGATAGCATCAGAAGAGCAGCAGCAAGTTCGGACAGTACAAAGAACGGT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  AGGAAGGCGGATGAAGATAGCATCAGAAGAGCAGCAGCAAGTTCGGACAGTACAAAGAACGGT 1140

Qy   1141  GATGGTACGAGCGCCCGTTTCGTCAGAACACACATGGTATCCGATGACATCCATCCAAG 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GATGGTACGAGCGCCCGTTTCGTCAGAACACACATGGTATCCGATGACATCCATCCAAG 1200

Qy   1201  AAACGAAGATCCCCAGATGAAGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AAACGAAGATCCCCAGATGAAGAACTGTTATACTTACCAGTGAGGGCCGTGAGACTTAT 1260

Qy   1261  GAAATGCTGTTGAAGATCAAAGAGTCCTGGAACTCATGCAGTCAGTACCTTCCTCAGCACACA 1320
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Db   1261  GAAATGCTGTTGAAGATCAAAGAGTCCTGGAACTCATGCAGTCAGTACCTTCCTCAGCACACA 1320

Qy   1321  ATTGAAACGTACAGGCAACACAGCAGCAGCCAGCACTTACTTCAGAAACATCTC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATTGAAACGTACAGGCAACACAGCAGCAGCCAGCACTTACTTCAGAAACATCTC 1380

Qy   1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTGTGAGCCCCGGAGAGAAACTCCAAAACAATCT 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTGTGAGCCCCGGAGAGAAACTCCAAAACAATCT 1440

Qy   1441  GACGTCTTCTTAGACATTCAAGCCCCAAACGATCAGTGTACCCCAAACGATCAGTGTACCCCTATC 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GACGTCTTCTTAGACATTCAAGCCCCAAACGATCAGTGTACCCCAAACGATCAGTGTACCCCTATC 1500

Qy   1501  TCTATATTTTAAGTGTGTGTTTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTGTA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  TCTATATTTTAAGTGTGTGTTTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTGTA 1560

Qy   1561  TGTGTGTGCGTGTATCGAGCCCTACAATCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TGTGTGTGCGTGTATCGAGCCCTACAATCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620

Qy   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAGGGACTCAAACCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAGGGACTCAAACCT 1680

Qy   1681  TTACAAGAAAGGATGTTTTCTGTGTTTCGTGTTTCGTTCTTAGACCCGGCCATTGGTGGTGAG 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TTACAAGAAAGGATGTTTTCTGTGTTTCGTGTTTCGTTCTTAGACCCGGCCATTGGTGGTGAG 1740

Qy   1741  GAACCACTGTGTTTGTCTGTGAGCTTTCTGTTCCTGGGAGGAGGGGTCAGGTGGG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAACCACTGTGTTTGTCTGTGAGCTTTCTGTTCCTGGGAGGAGGGGTCAGGTGGG 1800

Qy   1801  GAAAGGGCATTAAGATGTTTATTGGAACCCTTTCGTGTCTTCGTGTCTTGTGTTTTCTAA 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  GAAAGGGCATTAAGATGTTTATTGGAACCCTTTCGTGTCTTCGTGTCTTGTGTTTTCTAA 1860

Qy   1861  AATTCACAGGGAAGCTTTGAGCAGCTGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  AATTCACAGGGAAGCTTTGAGCAGCTGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920

Qy   1921  AAAAAAGTTGTTATTGCTGTGCATAAGTAAGTTGTCATAAGTAAGTTGTGTGTGACTGAGACTCAGTCAGA 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  AAAAAAGTTGTTATTGCTGTGCATAAGTAAGTTGTCATAAGTAAGTTGTGTGTGACTGAGACTCAGTCAGA 1980

Qy   1981  CCCTTTTAATGCTGCTGCATGTAATAATATTGCCAAGTAGTAGTAAGAAACGAAGGTGTCAAGTG 2040
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US-10-393-590-26

Query Match   100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TCGTTGATATCAAAGACAGTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TCGTTGATATCAAAGACAGTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT 60

Qy     61 ACAGTACTGCCCTGACCCTTACATCACCAGCGTTTCGTAGAAACCCAGCTCATTTCTTCTTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACAGTACTGCCCTGACCCTTACATCACCAGCGTTTCGTAGAAACCCAGCTCATTTCTTCTTGG 120

Qy    121 AAAGAAAGTTAATTACCGATCCACCATGTGTTGTTGGCCCCATAGCAGGTGAA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAGAAAGTTAATTACCGATCCACCATGTGTTGTTGGCCCCATAGCAGGTGAA 180

Qy    181 CCAGAGGTTTCCAGCATATCTGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGAGGTTTCCAGCATATCTGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240

Qy    241 ATTGACTTGAACTTGTGGATGAACATCAGAAGATGTGGACAAACAAGATTGAGATT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATTGACTTGAACTTGTGGATGAACATCAGAAGATGTGGACAAACAAGATTGAGATT 300

Qy    301 AGCATGATGACTGTATCCGCATGCCGTCGGACCTGGACCTGAGTGACCACCAGCAGTAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGCATGATGACTGTATCCGCATGCCGTCGGACCTGGACCTGAGTGACCACCAGCAGTAC 360

Qy    361 ACGAACCTGGGGCTCCTGACGACCACCAGCGCAGAACAGCGTCACGGCGCCCTCGCCTCGTCCACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACGAACCTGGGGCTCCTGACGACCACCAGCGCAGAACAGCGTCACGGCGCCCTCGCCTCGTCCACC 420

Qy    421 AGTCCCTATAACACAGACCAGCGCAGAACAGCGTCACGGCGCCCTACGCACAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTCCCTATAACACAGACCAGCGCAGAACAGCGTCACGGCGCCCTACGCACAG 480

Qy    481 CCCAGCTCCACCTTCGATGCTTCGACGTTTCGACGTGTCTTCCAACCGCCATCCCAACACCGACTAC 540
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Db    481 CCCAGCTCCACCTTCGATGCTTCGACGTTTCGACGTGTCTTCCAACCGCCATCCCAACACCGACTAC 540

Qy    541 CCAGGGCCGCCACAGTTTCGACGTGTCTTCGACGTCGGCCACC 600
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Db    541 CCAGGGCCGCCACAGTTTCGACGTGTCTTCGACGTCGGCCACC 600

Qy    601 TGGACGTATTCCACTGAACTCACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC 660
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Db    601 TGGACGTATTCCACTGAACTCACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC 660

Qy    661 CAGATCAAGGTGATGACGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAGATCAAGGTGATGACGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 720

Qy    721 AAAAAAGCTGAGCAGTTGTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780
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Db    721 AAAAAAGCTGAGCAGTTGTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780

Qy    781 GAATTCAACGAGGGACAGAGATTGCCCCTCCTAGTCATTTGATTCAGTAGAGGGGAACAGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GAATTCAACGAGGGACAGAGATTGCCCCTCCTAGTCATTTGATTCAGTAGAGGGGAACAGC 840

Qy    841 CATGCCCAGTATGTGAGATGTGAGAGATCCATCACAGGAAGACAGAGTGTGCTGGTGGTACTTATGAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGCCCAGTATGTGAGATGTGAGAGATCCATCACAGGAAGACAGAGTGTGCTGGTGGTACTTATGAG 900

Qy    901 CCACCCCAGGTTGGCACTGAATTCAGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCACCCCAGGTTGGCACTGAATTCAGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy    961 TGTGTTGGAGGGATGAACCGGCGTCCAATTTTAATCATTGTACTCTGGAAACCAGAGAT 1020
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Db    961 TGTGTTGGAGGGATGAACCGGCGTCCAATTTTAATCATTGTACTCTGGAAACCAGAGAT 1020
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Db   1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAAGAAACGAAGGTGTCAAGTG 2040

Qy   2041 TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC 2100

Qy   2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
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Db   2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160

Qy   2161 GCTGTGTACCTGCCTGCCACTGTATGTTGTTGGCATCTGTATGCTAAAGTTTTTCTTGTA 2220
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Db   2161 GCTGTGTACCTGCCTGCCACTGTATGTTGTTGGCATCTGTATGCTAAAGTTTTTCTTGTA 2220

Qy   2221 CATGAAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATGAAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280

Qy   2281 CTCATTTTGTGCTTTTAATAGAAAGACAAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CTCATTTTGTGCTTTTAATAGAAAGACAAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy   2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCCTCTCACAAAATCTGTGATT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCCTCTCACAAAATCTGTGATT 2400

Qy   2401 AATTTGCTTAATTAGAGCTTCTATCCCTCCAGCCTACCTACCATAAAAATCCAGCCATATTA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AATTTGCTTAATTAGAGCTTCTATCCCTCCAGCCTACCTACCATAAAAATCCAGCCATATTA 2460

Qy   2461 CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC 2520
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Db   2461 CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC 2520

Qy   2521 AGACCGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
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Db   2521 AGACCGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy   2581 TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCGTTTCTTTCCATTTAAAAACATATT 2640
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Db   2581 TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCGTTTCTTTCCATTTAAAAACATATT 2640

Qy   2641 TTAAGTAATAGCATAAAGACTTTAAAAATGTCCTCCCCCATCTTCCCACACCCAGT 2700
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Qy   2701 CACCAGCACTGTATTTTCTGTCAGGAAGACAAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760
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Db   2701 CACCAGCACTGTATTTTCTGTCAGGAAGACAAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760

Qy   2761 TTGTGGATGTGTGATTTAATTTTCAATAAACTTTGCATCTTGGTTAAATAAACTTTGCATCTTGGTTAAAAGAAA 2816
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Db   2761 TTGTGGATGTGTGATTTAATTTTCAATAAACTTTGCATCTTGGTTAAATAAACTTTGCATCTTGGTTAAAAGAAA 2816
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RESULT 6
US-10-393-590-26
; Sequence 26, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/366,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human

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Qy   1021 GGGCAAGTCCTGGGCCGACGCTGCTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGAC 1080
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Db   1021 GGGCAAGTCCTGGGCCCACGCTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGAC 1080

Qy   1081 AGGAAGGCGGATGAGAGAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGGAAGGCGGATGAGAGAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140

Qy   1141 GATGGTACGGAAGCGCCCGTTTCGTCAGAAACACACATGGTATCCAGATGACATCCATCAAG 1200
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Qy   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
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Db   1201 AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGACTTCCTCAGCACACA 1320
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Db   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGACTTCCTCAGCACACA 1320

Qy   1321 ATTGAAAACGTACAGGCAACAGCAACAGCAGCCACCACTTACTTCAGAAACATCTC 1380
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Db   1321 ATTGAAAACGTACAGGCAACAGCAACAGCAGCCACCACTTACTTCAGAAACATCTC 1380

Qy   1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT 1440

Qy   1441 GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC 1500

Qy   1501 TCTATATTTAAGTGTGTGTATTCCATGTGTATGTGAGTGTGTGTGTA 1560
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Db   1501 TCTATATTTAAGTGTGTGTATTCCATGTGTATGTGAGTGTGTGTGTA 1560

Qy   1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAGCACTTGGCTCAGAGA 1620
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Qy   1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACCT 1680
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Db   1681 TTACAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGGTGGGTGAG 1740

Qy   1741 GAACCACTGTGTTTGTCTGTGAGCTTTCTGTGTTGTTTCCTGTGTTTCTCGTTGTTTCTAA 1800
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Db   1741 GAACCACTGTGTTTGTCTGTGAGCTTTCTGTGTTGTTTCCTGTGTTTCTCGTTGTTTCTAA 1800

Qy   1801 GAAAGGGGCATTAAGAGTGTTATTGGAACCCTTTCTCGTCTTCTCGTTGTTTTCTAA 1860
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Db   1801 GAAAGGGGCATTAAGAGTGTTATTGGAACCCTTTCTCGTCTTCTCGTTGTTTTCTAA 1860

Qy   1861 AATTCACAGGGAAGCTTTGTTGTCATAAGTAAGTTGTAGGTGACTGAGAAAAGGAG 1920
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Db   1861 AATTCACAGGGAAGCTTTGTTGTCATAAGTAAGTTGTAGGTGACTGAGAAAAGGAG 1920

Qy   1921 AAAAAAGTTGTTATTGTTGTCTGTGCATAAGTAAGTAAGTGCAAGTGACTAGAGAACGAGGTGTCAAGTG 1980
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Db   1921 AAAAAAGTTGTTATTGTTGTCTGTGCATAAGTAAGTAAGTGCAAGTGACTAGAGAACGAGGTGTCAAGTG 1980

Qy   1981 CCCTTTTAATGCTGTCATGCATGTAATAATATATTGCAAGTAGTAGTAAGAAACGAGGTGTCAAGTG 2040
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Db   1981 CCCTTTTAATGCTGTCATGCATGTAATAATATATTGCAAGTAGTAGTAAGAAACGAGGTGTCAAGTG 2040

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Db   2041 TACTGCTGGGCAGCCAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGAGTTC 2100
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Qy   2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCATGTGTAGGTAGAAGACATTCTTAAT 2160
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Db   2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCATGTGTAGGTAGAAGAACATTCTTAAT 2160

Qy   2161 GCTGTGTACCTGCCCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
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Db   2161 GCTGTGTACCTGCCCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220

Qy   2221 CATGAAACCCTGGAAGACCTACTACACAAAAAACTGTGTTGGTGTTGGCGCCCATAGCAGGTGAA 2280
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Db   2221 CATGAAACCCTGGAAGACCTACTACACAAAAAACTGTGTTGGTGTTGGCGCCCATAGCAGGTGAA 2280

Qy   2281 CTCATTTGTGCTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340
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Db   2281 CTCATTTTGTGCTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy   2341 TGTTTACCATTATTCAAAGTCAAAATAGAATTTGAAGCCCTCTCCACAAAATCTGTGATT 2400
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Db   2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCTCTCCACAAAATCTGTGATT 2400

Qy   2401 AATTTGCTTAATTAGAGCTTCTATCCCTCAGCCTACTTACCATCATAAAAACCAGCCATATTA 2460
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Db   2401 AATTTGCTTAATTAGAGCTTCTATCCCTCAGCCTACTTACCATCATAAAAACCAGCCATATTA 2460

Qy   2461 CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC 2520

Qy   2521 AGACGTGTTAAAATCAGCACTCCTGACTGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
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Db   2521 AGACGTGTTAAAATCAGCACTCCTGACTGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy   2581 TTCTTTTTTTACTCAAAAGTTAGAGAATCCTGTTTCTTTCCATTTTAAAAACATATT 2640
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Db   2581 TTCTTTTTTTACTCAAAAGTTAGAGAATCCTGTTTCTTTCCATTTTAAAAACATATT 2640

Qy   2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCATCTTCCCACACCCAGT 2700
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Db   2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCATCTTCCCACACCCAGT 2700

Qy   2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT 2760

Qy   2761 TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTCGCATCTTGGTTTAAAAGAAA 2816
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Db   2761 TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTCGCATCTTGGTTTAAAAGAAA 2816
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Query Match              100.0%;  Score 2816;  DB 16;  Length 2816;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 2816;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT    60
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Db      1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCT    60

Qy     61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTCGTAGAAACCCAGCTCATTTCTCTTGG   120
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Db     61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTCGTAGAAACCCAGCTCATTTCTCTTGG   120

Qy    121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCGAT   180
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Db    121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT   180

Qy    181 CCAGAGTTTTCCAGCATATCTGGGATTTTCTGGACAGCCTATATGTTCAGTTCAGCCCC   240
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Db    181 CCAGAGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCC   240

Qy    241 ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT   300

Qy    301 AGCATGACTGTATCCGCATCGAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC   360
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Db    301 AGCATGACTGTATCCGCATCGAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC   360

Qy    361 ACGAACCTGGGGCTCCTGAACAGCAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACGAACCTGGGGCTCCTGAACAGCAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC   420

Qy    421 AGTCCCTATAACACAGACCACAGCGTCACGGCCCTCGCCCTACGCACACAG   480
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Db    421 AGTCCCTATAACACAGACCACAGCGCGCAGAACAGCGCCCTCGCCCTACGCACACAG   480

Qy    481 CCCAGCTCCACCTTGATGTCTTCCTCCATCCCCCGCACCCCATCCCCTGTCTAC   540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCCAGCTCCACCTTCGATGCTCTCTCCATCCCCTCCATCCCCTGTCTAC   540

Qy    541 CCAGGCCCGCACAGTTCGACGTCTTCGAGCGTGGAAGTCGGAGCACCGGCCACC   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCAGGCCCGCACAGTTCGACGTCTTCGAGCGTCGAGCAGTCGAGCCCGGCCACC   600

Qy    601 TGGACGTATTCCACTGAACTCTACTGCCCATCTACTGCCAAATTGCAAAGACATGCCCCATC   660
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Db    601 TGGACGTATTCCACTGAACTCTACTGCCCATCTACTGCCAAATTGCAAAGACATGCCCCATC   660

Qy    661 CAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTCAGGAGCTGTTATCCGCGGCATGCCTGTCTAC   720
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Db    661 CAGATCAAGGTGATGACCCACCTCCTCAGGGAGCTCAGGAGCTGTTATCCGCGGCATGCCTGTCTAC   720

Qy    721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCCGTGAAGCCGTGGTCTGAGCTGAGCTGAGCCGT   780
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Db    721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCCGTGAAGCCGTGGTCTGAGCTGAGCCGT   780

Qy    781 GAATTCAACGAGGGGACAGATGCCCCTCCAGTCAATTTTTAATCATTGTTACTCTGGAAACCAGACAGC   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GAATTCAACGAGGGGACAGATGCCCCTCCAGTCAATTTTTAATCATTGTTACTCTGGAAACCAGACAGC   840

Qy    841 CATGCCAAGGTAGAGAATGTGAGAGATCCCATCACAGAAGAACAGAGTGTCGGGTACCTTATGAG   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CATGCCAAGGTAGAGAATGTGAGAGATCCCATCACAGAAGAACAGAGTGTCGGGTACCTTATGAG   900

Qy    901 CCACCCCAGGTTGGCACTGAATTCACGACACAGTGCTTGTACAATTTCATGTGTAACAGCAGT   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CCACCCCAGGTTGGCACTGAATTCACGACACAGTGCTTGTACAATTTCATGTGTAACAGCAGT   960

Qy    961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGTGTTGGAGGGATGAACCGCCGTCCAATTTTTAATCATTGTTACTCTGGAAACCAGAGAT  1020

Qy   1021 GGGCAAGTCCTGGGCCGACGCGTCTTTGAGGCCCGGACCTGCTTTGCCCAGGAAGGAGAGAC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGGCAAGTCCTGGGCCGACGCGTCTTTGAGGCCCGGACCTGCTTTGCCCAGGAAGGAGAGAC  1080

Qy   1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT  1140
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Db   1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1141 GATGGTACGAAGCGCCCGTTTCGTCAGAACACACACATGGTATCCGATGACGACATCCATCAAG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGGTACGAAGCGCCCGTTTCGTCAGAACACACACATGGTATCCGATGACGACATCCATCAAG  1200

Qy   1201 AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGACGGCCGTGAGACTTAT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGGCCGTGAGACTTAT  1260

Qy   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAACTCATGTCAGTACCTTCCTCAGCACACACA  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGAACTCATGTCAGTACCTTCCTCAGCACACA  1320

Qy   1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACATCATCTC  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATTGAAACGTACAGGCAACAGCAACAGCAGCACCAGCACTTACTTCAGAAACATCATCTC  1380

Qy   1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440

Qy   1441 GACGTCTCTTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACGTCTCTTTTAGACATTCCAAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500

Qy   1501 TCTATATTTTAAGTGTGTGTTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGTGTGTA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TCTATATTTTAAGTGTGTGTTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGTGTGTA  1560

Qy   1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA  1620

Qy   1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAATCTTTTGAAGGGACTCAAACCT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAATCTTTTGAAGGGACTCAAACCT  1680

Qy   1681 TTACAAGAAAGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGGGTGGTGAG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TTACAAGAAAGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGGGTGGTGAG  1740

Qy   1741 GAACCACTGTGTTTGTCTGTGAGCTTTCGTGTTGTTCCTGGGGAGGGGGTCAGGTGGG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GAACCACTGTGTTTGTCTGTGAGCTTTCGTGTTGTTCCTGGGGAGGGGGTCAGGTGGG  1800

Qy   1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTCTGTGTTTTTCTAA  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTCTGTGTTGTTTTTCTAA  1860

Qy   1861 AATTCACAGGAAGCTTTGAGCAGTTCGTGTGCATAAGTAAGTGTGTACTGAGACTCAGTCAGA  1920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AATTCACAGGAAGCTTTGAGCAGTTCGTGTGCATAAGTAAGTGTGTACTGAGACTCAGTCAGA  1920

Qy   1921 AAAAAAGTTGTTATTGTCGTGTGCATAATAATATTGCAAGTAGTAGTAAGAACGAAGGTGTCAAGTG  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AAAAAAGTTGTTATTGTCGTGTGCATAATAATATTGCAAGTAGTAGTAAGAACGAAGGTGTCAAGTG  1980

Qy   1981 CCCTTTTAATGCTGGTGGTCATGTAATAATATTCATGTGTAACAGCAGT  2040
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CCCTTTTAATGCTGGTGGTCATGTAATAATATTCATGTGTAACAGCAGT  2040

Qy   2041 TACTGCTGGCAGCGAGCTGAGTGATCATTACCAAAAGTAATCAACTTTGTGGGGAGTTC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TACTGCTGGCAGCGAGCTGAGTGATCATTACCAAAAGTAATCAACTTTGTGGGGAGTTC  2100

Qy   2101 TTTGTGAGAACTTGCATTATTTGTCTCCCCCATGTAGTAGTAGAACATTTCTTAAT  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTTGTGAGAACTTGCATTATTTGTCTCCCCCATGTAGTAGTAGAACATTTCTTAAT  2160

Qy   2161 GCTGTGTACCTCGCCTCTGCCACTGTAGTGGCATCGTGTTATGTCTGTAAAGTTTTTCTTGTA  2220
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Db    61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120

Qy   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGACACAGACAAATGAATTCCTCAGT   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGACACAGACAAATGAATTCCTCAGT   180

Qy   181  CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGTTCAGCCC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGTTCAGCCC   240

Qy   241  ATTGACTTGAACTTTGTGGATGAACCATCGAAAGTGTGCGACAAACAAGATTGAGATT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATTGACTTGAACTTTGTGGATGAACCATCGAAAGTGTGCGACAAACAAGATTGAGATT   300

Qy   301  AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTGCACCTGGCCACAGTAC     360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGCATGGACTGTATCCGCATGCAGGACTCGGACCTGAGTGCACCTGGCCACAGTAC     360

Qy   361  ACGAACCTGGGCTCCTGAACAGCAGCCAGCAGATTCAGACGCTCTCGTCCGTCCGTCCACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACGAACCTGGGCTCCTGAACAGCAGCCAGCAGATTCAGACGCTCTCGTCCGTCCGTCCACC 420

Qy   421  AGTCCCTATAACACAGACACACGCGCAGAACACAGCGTCACGGGGCCCTCGCCCTACGGCACAG 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AGTCCCTATAACACAGACACACGCGCAGAACACAGCGTCACGGGGCCCTCGCCCTACGGCACAG 480

Qy   481  CCCAGCTCCACCTTCGATGCTCTCTCCAATCACCCGCCATCCCATCCCAACACCGACTAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CCCAGCTCCACCTTCGATGCTCTCTCCAATCACCCGCCATCCCATCCCAACACCGACTAC  540

Qy   541  CCAGGCCCGCACAGTTCGACGTGTCTTCCAGCAGTCGAGCAGTGTCGGCCGCACC       600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CCAGGCCCGCACAGTTCGACGTGTCTTCCAGCAGTCGAGCAGTGTCGGCCGCACC       600

Qy   601  TGGACGTATTCCACTGAACTGAAGAAACTTACTGCAAATTGCAAAGACATGCCCCATC    660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGGACGTATTCCACTGAACTGAAGAAACTTACTGCAAATTGCAAAGACATGCCCCATC    660

Qy   661  CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCTGTCTAC    720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCTGTCTAC    720

Qy   721  AAAAAGCTGAGCACGTCACGGAGCGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGGT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AAAAAGCTGAGCACGTCACGGAGCGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGGT  780

Qy   781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCAGTAGAGGGGAACAGC  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCAGTAGAGGGGAACAGC  840

Qy   841  CATGCCCAGTATGTGAGAAGATCCCATCACAGGAAGACAGAGTGTCGTGGTACCTTATGAG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CATGCCCAGTATGTGAGAAGATCCCATCACAGGAAGACAGAGTGTCGTGGTACCTTATGAG 900

Qy   901  CCACCCCAGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CCACCCCAGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960

Qy   961  TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTACTCTGGAAACCAGAGAT    1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTACTCTGGAAACCAGAGAT    1020

Qy  1021  GGGCAAGTCCTGGGCCGCAGCGCTGCTTTGAGGCCCGACCAAGAGAGCAACAGC       1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGGCAAGTCCTGGGCCGCAGCGCTGCTTTGAGGCCCGACCAAGAGAGCAACAGC       1080

Qy  1081  AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT   1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT   1140

Qy  1141  GATGGTACGAAGCGCGCCCGTTTCGTCAGAACACACATGACATCCATCAAG        1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GATGGTACGAAGCGCGCCCGTTTCGTCAGAACACACATGACATCCATCAAG        1200
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Db  2161  GCTGTGTACCTGCCCTGCCCACGTATGTTGGCATCTGTATGCTAAAGTTTTCTTGTA    2220

Qy  2221  CATGAAAACCTGGAAGAACTACTACAAAAAACTGTTGTTGTTGGCCCCATAGCAGGTGAA  2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CATGAAAACCTGGAAGAACTACTACAAAAAACTGTTGTTGTTGGCCCCATAGCAGGTGAA  2280

Qy  2281  CTCATTTGTGCTTTAATAGAAGACAAATCACCCAGTAATCCAGTTACGTAGT         2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CTCATTTGTGCTTTAATAGAAGACAAATCACCCAGTAATCCAGTTACGTAGT         2340

Qy  2341  TGTTTACCATTATTCAAAGCTCAAATAGAATTCAAAGCCCTCTCACAAAATCTGTGATT   2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  TGTTTACCATTATTCAAAGCTCAAATAGAATTCAAAGCCCTCTCACAAAATCTGTGATT   2400

Qy  2401  AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCTTCCATACCATAAAAACCAGCCATATTA  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  AATTTGCTTAATTAGAGCTTCTATCCCTCAAGCTTCCATACCATAAAAACCAGCCATATTA  2460

Qy  2461  CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC   2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC   2520

Qy  2521  AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT   2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT   2580

Qy  2581  TCTTTTTTTTACTCAAAAGTTTAGGAGAATCTCGTTCTTCCATTTTAAAAACATATT      2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  TCTTTTTTTTACTCAAAAGTTTAGGAGAATCTCGTTCTTCCATTTTAAAAACATATT      2640

Qy  2641  TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCATCTTCCCACACCCAGT      2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCATCTTCCCACACCCAGT      2700

Qy  2701  CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTTGTTATTGGGCTGTTGCTT    2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTTGTTATTGGGCTGTTGCTT    2760

Qy  2761  TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTGCATCTGTTTGGTTTAAAAGAAA   2816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTGCATCTGTTTGGTTTAAAAGAAA   2816
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Query Match     100.0%;  Score 2816;  DB 16;  Length 2816;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2816;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAACTTCACGGTGTGCCACCCT    60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAACTTCACGGTGTGCCACCCT    60

Qy    61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GATGGTACGAAGCGCGCCCGTTTCGTCAGAACACACATGACATCCATCAAG
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Qy   1201  AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGGCCGTGAGACTTAT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AAACGAAGATCCCCAGATGATGAACTGTATACTTACCAGTGAGGGGCCGTGAGACTTAT  1260

Qy   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCAGTAGCACTCCTCCAGCACACA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCAGTAGCACTCCTCCAGCACACA  1320

Qy   1321  ATTGAAACGTACAGGCAACAGCAGCAGCCACCAGCACTTACTTCAGAAAACATCTC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATTGAAACGTACAGGCAACAGCAGCAGCCACCAGCACTTACTTCAGAAAACATCTC  1380

Qy   1381  CTTTCAGCCTGCTTCAGGAAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTTTCAGCCTGCTTCAGGAAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440

Qy   1441  GACGTCTCTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCCTATC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GACGTCTCTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCCTATC  1500

Qy   1501  TCTATATTTTAAGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTA  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  TCTATATTTTAAGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTA  1560

Qy   1561  TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA  1620

Qy   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT  1680

Qy   1681  TTACAAGAAAGGATGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TTACAAGAAAGGATGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy   1741  GAACCACTGTGTTGTGTCTGTGAGCTTCTGTGTTCCTGGAGGGAGGGGTCAGGTGGG  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAACCACTGTGTTGTGTCTGTGAGCTTCTGTGTTCCTGGAGGGAGGGGTCAGGTGGG  1800

Qy   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCCTTTCGTCTTCTTCGTGTTGTTTTCTAA  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCCTTTCGTCTTCTTCGTGTTGTTTTCTAA  1860

Qy   1861  AATTCACAGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  AATTCACAGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920

Qy   1921  AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTGTAGGTGACTGAGAGACTCAGTCAGA  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTGTAGGTGACTGAGAGACTCAGTCAGA  1980

Qy   1981  CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAAGTAAGAAACGAAGGTGTCAAGTG  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAAGTAAGAAACGAAGGTGTCAAGTG  2040

Qy   2041  TACTGCTGGGCAGCGAGGTGATCATTTTGTGTCCTCCCCCATGTGTAGGTAGAACATTTCTTAAT  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TACTGCTGGGCAGCGAGGTGATCATTTTGTGTCCTCCCCCATGTGTAGGTAGAACATTTCTTAAT  2100

Qy   2101  TTTGTGAGAACTTGCATTATTTTGTGTCCCCTCCATGTGTAGGTAGGTAGAACATTTCTTAAT  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TTTGTGAGAACTTGCATTATTTTGTGTCCCCTCCATGTGTAGGTAGGTAGAACATTTCTTAAT  2160

Qy   2161  GCTGTGTACCTGCCCCTGCCTCTGCCACTGTATGCTGCCATCGTATTATGCTAAAGTTTTTCTTGTA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCTGTGTACCTGCCCCTGCCTCTGCCACTGTATGCTGCCATCGTATTATGCTAAAGTTTTTCTTGTA  2220

Qy   2221  CATGAAACCCTGAAGACTTGGCCCCCATAGCAGGTGAA  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CATGAAACCCTGAAGACTTGGCCCCCATAGCAGGTGAA  2280


Qy   2281  CTCATTTGTGCTTTAATAGAAAGACAAATCACCCCAGTAATATTGCCCTTACGTAGT  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTCATTTGTGCTTTAATAGAAAGACAAATCACCCCAGTAATATTGCCCTTACGTAGT  2340

Qy   2341  TGTTTACCATTATTCAAAGCTCAAAGCTCAAAGCTCAAATAGAATTGAAGCCCTCTCACAAAATCTGTGATT  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  TGTTTACCATTATTCAAAGCTCAAAGCTCAAAGCTCAAATAGAATTGAAGCCCTCTCACAAAATCTGTGATT  2400

Qy   2401  AATTGCTAATTAGAGCTTCTATCCCTCAAGCTACCTACCTACCATAAAAACCAGCCATATTA  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  AATTGCTAATTAGAGCTTCTATCCCTCAAGCTACCTACCTACCATAAAAACCAGCCATATTA  2460

Qy   2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC  2520

Qy   2521  AGACGTGTTAAAATCAGACTCCTGGACTGGAAATTAAAGATTAAAGGGTAGACTACTT  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  AGACGTGTTAAAATCAGACTCCTGGACTGGAAATTAAAGATTAAAGGGTAGACTACTT  2580

Qy   2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATATT  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATATT  2640

Qy   2641  TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCCATCTTCCCACACCCAGT  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCCATCTTCCCACACCCAGT  2700

Qy   2701  CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTGTTATTGGGCTGTTGCTT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTGTTATTGGGCTGTTGCTT  2760

Qy   2761  TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTCAATAAACTTTGCATCTTGGTTTAAAAGAAA  2816
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTCAATAAACTTTGCATCTTGGTTTAAAAGAAA  2816
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RESULT 9
US-10-393-590-65
; Sequence 65, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: human
US-10-393-590-65

Query Match   100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity   100.0%;
Matches 2816; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCAGCGGTGTGCCACCCT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCAGCGGTGTGCCACCCT  60

Qy    61  ACAGTACTGCCCTGACCCTGACCCTTACATCCAGCGTTCGTAGAACCCAGCTCATTCTTCTTGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ACAGTACTGCCCTGACCCTGACCCTTACATCCAGCGTTCGTAGAACCCAGCTCATTCTTCTTGG  120

Qy   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACACCACAGACACAATGAATTCCTCAGT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACACCACAGACACAATGAATTCCTCAGT  180
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Qy   181  CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240

Qy   241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300

Qy   301  AGCATGACTGTATCCGCATCGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGCATGACTGTATCCGCATCGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC  360

Qy   361  ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTGTCCACC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTGTCCACC  420

Qy   421  AGTCCCTATAACACAGACCACGCGCAGAACAGCGTCACGGGCGCCCTGCCCTACCGCACAG  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AGTCCCTATAACACAGACCACGCGCAGAACAGCGTCACGGGCGCCCTGCCCTACCGCACAG  480

Qy   481  CCCAGTCCACCTTGATGTCTCCATCACCGCCATCCCCTCCAACACCGACTAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CCCAGTCCACCTTCGATGTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC  540

Qy   541  CCAGGCCCGCACAGTTCGACGTGTCCTTCGCAGCAGTCGAGCACGTCGGCGCCACC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CCAGGCCCGCACAGTTCGACGTGTCCTTCGCAGCAGTCGAGCACGTCGGCGCCACC  600

Qy   601  TGGACGTATTCCACTGAACTCTACTGCCAAATTGCAAAGACATGCCCCATC  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGGACGTATTCCACTGAACTCTACTGCCAAATTGCAAAGACATGCCCCATC  660

Qy   661  CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTATCCGCCGCCATGCCTGCTAC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CAGATCAAGGTGATGACCCCACCTCCTCAGGGAGCTGTATCCGCCGCCATGCCTGCTAC  720

Qy   721  AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT  780

Qy   781  GAATTCAACGACAGATTGCCCCTCCAGTCATTTGATTCGAGTAGAGGGGAACAGC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GAATTCAACGACAGATTGCCCCTCCAGTCATTTGATTCGAGTAGAGGGGAACAGC  840

Qy   841  CATGCCCAGTATGTAGAAGATGTGAGAAGACAGAGTGTGCTGGTACCTTATGAG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CATGCCCAGTATGTAGAAGATGTGAGAAGACAGAGTGTGCTGGTACCTTATGAG  900

Qy   901  CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960

Qy   961  TGTGTTGGAGGGATGAACCGCGCCGTCTTGAGGGCCCGGATCTGCTTGCCCCAGGAGGAC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TGTGTTGGAGGGATGAACCGCGCCGTCTTGAGGGCCCGGATCTGCTTGCCCCAGGAGGAC  1020

Qy  1021  GGGCAAGTCCTGGGCCACGCCGTCTTGAGGGCCCGGATCTGCTTGCCCCAGGAGGAGAC  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGGCAAGTCCTGGGCCACGCCGTCTTGAGGGCCCGGATCTGCTTGCCCCAGGAGGAGAC  1080

Qy  1081  AGGAAGGCGGATGAAGATAGCACATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGT  1140
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Db  1081  AGGAAGGCGGATGAAGATAGCACATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT  1140

Qy  1141  GATGGTACGGAAGCGCCCCGTTCGTCAGAACACACACATGGTATCCAGATGACATCCATCAAG  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GATGGTACGGAAGCGCCCCGTTCGTCAGAACACACACATGGTATCCAGATGACATCCATCAAG  1200

Qy  1201  AAACAAGAGATCCCCAGATGATGAAGATCCCCAGATGATGAAGGGCCGTGAGGGCCGTGAGACTTAT  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  AAACAAGAGATCCCCAGATGATGAACTGTTATATACTTACCAGTGACAGTGAGGGCCGTGAGACTTTAT  1260

Qy  1261  GAAATCGTGTTGAAGATCAAAGATCCCTGGAACTCAAGAGTCCTGGAACTCAGCAGTACCTTCCTCAGCACACA  1320
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Db  1261  GAAATCGTGTTGAAGATCAACAAGAGTCCCTGGAACTCAGCAGTACCTTCCTCAGCACACA  1320

Qy  1321  ATTGAAACGTACAGGCAACAGCAGCAACAGCAGCACCAGCACCACTTACTTCAGAAACATCTC  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ATTGAAACGTACAGGCAACAGCAGCAACAGCAGCACCAGCACCACTTACTTCAGAAACATCTC  1380

Qy  1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAAACTCCAAAACAATCT  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAAACTCCAAAACAATCT  1440

Qy  1441  GACGTCTTCTTTGACATTCCAGCCCCAAACCGATCAGTGTACCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GACGTCTTCTTTGACATTCCAGCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500

Qy  1501  TCTATATTTAAGTGTGTGTTGTATTCCATGTGTATTCCATGTGTGTATGTGAGTGTGTGTGTGTA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  TCTATATTTAAGTGTGTGTTGTATTCCATGTGTATTCCATGTGTGTATGTGAGTGTGTGTGTGTA  1560

Qy  1561  TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTGGCTCAGAGA  1620

Qy  1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAACCT  1680

Qy  1681  TTACAAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  TTACAAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy  1741  GAACCACTGTGTTGTCGTGTGAGCTTTCTGTTTCCTGGGAGGGGGTCAGGTGGG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GAACCACTGTGTTGTCGTGTGAGCTTTCTGTTTCCTGGGAGGGGGTCAGGTGGG  1800

Qy  1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCGTCTCTTCGTCTCTTCTTCTTAA  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCGTCTCTTCGTCTCTTCTTCTTAA  1860

Qy  1861  AATTCACAGGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  AATTCACAGGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920

Qy  1921  AAAAAAGTTGTTATTGCTGTGCATAAGTAAGTTGTAGGTAGTAAGAGAACTCAGTCAGA  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  AAAAAAGTTGTTATTGCTGTGCATAAGTAAGTTGTAGGTAGTAAGAGAACTCAGTCAGA  1980

Qy  1981  CCCTTTTAATGCTGTCATGTAATATATTCAAGAGTAAGAGTAAGAAAACGAAGGTGTCAAGTG  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CCCTTTTAATGCTGGTCATGTAATATATTCAAGAGTAAGAGTAAGAAAACGAAGGTGTCAAGTG  2040

Qy  2041  TACTGCTGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGGAGTTC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TACTGCTGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGGAGAGTTC  2100

Qy  2101  TTTGTGAGAACTTGCATTATTTGTCTCCCCTCATGTGTAGGTAGTAGGTAGTAACATTTCTTAAT  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  TTTGTGAGAACTTGCATTATTTGTCTCCCCTCATGTGTAGGTAGTAGGTAGTAACATTTCTTAAT  2160

Qy  2161  GCTGTGTACCTGCCTCTGCCACTGTGTTGGCATCTGTTATGCTAAAGTTTTTTCCTTGTA  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCTGTGTACCTGCCTCTGCCACTGTGTTGGCATCTGTTATGCTAAAGTTTTTTCCTTGTA  2220

Qy  2221  CATGAAACCCTGGAAGACCTACTACACAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CATGAAACCCTGGAAGACCTACTACACAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA  2280

Qy  2281  CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCCAGTAATATTGCCCTTACGTAGT  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCCAGTAATATTGCCCTTACGTAGT  2340

Qy  2341  TGTTTACCATTATTCAAAGCTCAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   241  ATTGACTTGAACTTGTGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300

Qy   301  AGCATGGACTGTATCCGCATGCAGGACTCGGACTGAGTGAGTGCCAGTACC  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AGCATGGACTGTATCCGCATGCAGGACTCGGACTGAGTGAGTGCCAGTAC  360

Qy   361  ACGAACTTGGGGCTCCTGACACGATGGACAGCAGAGATTCAGAACGGCTCCGTCCACC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  ACGAACTTGGGGCTCCTGACACGATGGACAGCAGAGATTCAGAACGGCTCCGTCCACC  420

Qy   421  AGTCCCTATAACACAGACCACGCGCAGAACACAGGGTCACGCGCCCTCGCCCTACGCACAG  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AGTCCCTATAACACAGACCACGCGCAGAACACAGCGTCACGCGCCCTCGCCCTACGCACAG  480

Qy   481  CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCCTCCAACACCGACTAC  540

Qy   541  CCAGGCCCCACAGTTTCGAGGTGTCCTTCGAGTGCAGTGCGACTCGGCCACC  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  CCAGGCCCCACAGTTTCGAGGTGTCCTTCGAGTGCAGTGCGACTCGGCCACC  600

Qy   601  TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAATGCAATGCCCCATC  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAATGCAATGCCCCATC  660

Qy   661  CAGATCAAGGTGATGACCCCACCTCCTCAGGAGTGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT  720
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CAGATCAAGGTGATGACCCCACCTCCTCAGGAGTGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT  720

Qy   721  AAAAAGCTGAGCACGTCACGGACGTGCCCTCGAGTGGAACAGC  780
          |||||||||||||||||||||||||||||||||||||||||||
Db   721  AAAAAGCTGAGCACGTCACGGACGTGCCCTCGAGTGGAACAGC  780

Qy   781  GAATTCAACGAGGGACAGATTGCCCTCCTAGTCATTTGATTCGAGTAGGAGGGAACAGC  840
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GAATTCAACGAGGGACAGATTGCCCTCCTAGTCATTTGATTCGAGTAGGAGGGAACAGC  840

Qy   841  CATGCCCAGTATGTGAGAGATGAGAAGACAGCAGAGTGTGCTGGTGTACCTTATGAG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CATGCCCAGTATGTGAGAGATGAGAAGACAGCAGAGTGTGCTGGTGTACCTTATGAG  900

Qy   901  CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTCATGTGTAACAGCAGT  960
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTCATGTGTAACAGCAGT  960

Qy   961  TGTGTTGGAGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  TGTGTTGGAGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT  1020

Qy  1021  GGGCAAGTCCTGGCCGACGCGCTTGCTTTGAGGCCCGGATCGTTGCCCAGGAAGGAGAC  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGGCAAGTCCTGGCCGACGCGCTTGCTTTGAGGCCCGGATCGTTGCCCAGGAAGGAGAC  1080

Qy  1081  AGGAAGGCGGATGAAGATAGCATCAGAAGCAGCAAGTTCGGACAGTACAAAGAACGGT  1140
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  AGGAAGGCGGATGAAGATAGCATCAGAAGCAGCAAGTTCGGACAGTACAAAGAACGGT  1140

Qy  1141  GATGGTACGAAGCGCGCCGTTTCGTCAGAACACACATGTATCCAGATGACATCCATCAAG  1200
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  GATGGTACGAAGCGCGCCGTTTCGTCAGAACACACATGTATCCAGATGACATCCATCAAG  1200

Qy  1201  AAACGAAGATCCCAGATGATGAACGTTATACTTACCAGTGAGGGGCGTGAGACTTAT  1260
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  AAACGAAGATCCCAGATGATGAACGTTATACTTACCAGTGAGGGGCGTGAGACTTAT  1260

Qy  1261  GAAATGCTGTTGAAGATCAAAGAGTCAAGGCCCTATATGTTCAGTTCAGCGCC  1320
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GAAATGCTGTTGAAGATCAAAGAGTCAAGGCCCTATATGTTCAGTTCAGCGCC  1320

Qy  1321  ATTGAAACGTACAGGCAACAGCAACAGCAGCACACTTACTTCAGAAACATCTC  1380
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  ATTGAAACGTACAGGCAACAGCAACAGCAGCACACTTACTTCAGAAACATCTC  1380
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Db  2341  TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400

Qy  2401  AATTTGCTTAATTAGAGAGCTTCATCCTCAAGCCTACCTACCATAAAACCAGCCATATTA  2460
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  AATTTGCTTAATTAGAGAGCTTCATCCTCAAGCCTACCTACCATAAAACCAGCCATATTA  2460

Qy  2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTAGCGTTTTGAGTAAGTGAGATCCAAGC  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTAGCGTTTTGAGTAAGTGAGATCCAAGC  2520

Qy  2521  AGACGTGTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT  2580
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  AGACGTGTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT  2580

Qy  2581  TTCTTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATATT  2640
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  TTCTTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATATT  2640

Qy  2641  TTAAGATAATAGCATAAAGACTTTAAAAAATGTTCCTCCCCCATCTTCCCACACCCAGT  2700
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TTAAGATAATAGCATAAAGACTTTAAAAAATGTTCCTCCCCCATCTTCCCACACCCAGT  2700

Qy  2701  CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT  2760
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTTGCTT  2760

Qy  2761  TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA  2816
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA  2816
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RESULT 10
US-10-393-567-26
; Sequence 26, Application US/10393567
; Publication No. US2003019473A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-26

Query Match   100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2816; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT  60
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Db     1  TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT  60

Qy    61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTGAAACCCAGCTCATTTCTCTTGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTGAAACCCAGCTCATTTCTCTTGG  120

Qy   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT  180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGACAAATGAATTCCTCAGT  180

Qy   181  CCGAGAGGTTTTTCCAGCATATCTGGGATTTCTGGGATTTCTGGAACAGCCCTATATGTTCAGCCC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  CCGAGAGGTTTTTCCAGCATATCTGGGATTTCTGGGATTTCTGGAACAGCCCTATATGTTCAGCCC  240

Qy   241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  ATTGACTTGAACTTGTGGATGAACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT  300
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Qy  2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGTAGTAAGTGAGATCCAAGC  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGTAGTAAGTGAGATCCAAGC  2520

Qy  2521  AGACGTGTTAAAATCAGCACTCCTGACTGAACTGAAAATAAAGATTGAAAGGGTAGACTACTT  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  AGACGTGTTAAAATCAGCACTCCTGACTGAACTGAAAATAAAGATTGAAAGGGTAGACTACTT  2580

Qy  2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTCTTCCATTTTAAAAACATATT  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTCTTCCATTTTAAAAACATATT  2640

Qy  2641  TTAAGATAATAGCATAAAGACTTAAAAATGTTCCTCCCCTCCATCTTCCCACACCCAGT  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TTAAGATAATAGCATAAAGACTTAAAAATGTTCCTCCCCTCCATCTTCCCACACCCAGT  2700

Qy  2701  CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTGTATTGAGCGTGTTGCTT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTGTATTGAGCGTGTTGCTT  2760

Qy  2761  TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA  2816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA  2816
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RESULT 11
US-10-393-567-27
; Sequence 27, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 2816
;   TYPE: DNA
;   ORGANISM: human
US-10-393-567-27

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Query Match       100.0%;  Score 2816;  DB 16;  Length 2816;
Best Local Similarity 100.0%;
Matches 2816;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  TCGTTGATATCAAAGACAGTGAAGAAATGAAATTTGAAACTTCACGGTGTGCCACCCT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  TCGTTGATATCAAAGACAGTGAAGAAATGAAATTTGAAACTTCACGGTGTGCCACCCT   60

Qy   61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCAGCACAGAGAAATGAATT   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCAGCACAGAGAAATGAATT   120

Qy  121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGACACACAGAGATTCCTCAGT   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGACACACAGAGATTCCTCAGT   180

Qy  181  CCGAGAGTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGCGC   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CCGAGAGTTTCCAGCATATCTGGGATTTCTGGAACAGCCTATATGTTCAGCGC   240

Qy  241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGTGCCACAAACAAGATTGAGATT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  ATTGACTTGAACTTTGTGGATGAACCATCAGAAGATGTGCCACAAACAAGATTGAGATT   300

Qy  301  AGCATGGACTGTATCCGCATGCAGGACTCGGACTCGGAGCCCATGTGACCCGAGTGACCAGTAC   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  AGCATGGACTGTATCCGCATGCAGGACTCGGACTCGGAGCCCATGTGACCCGAGTGACCAGTAC   360
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Qy  1381  CTTTCAGCCTGCTTCTTCAGGAATGAGCTTGTGTGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CTTTCAGCCTGCTTCTTCAGGAATGAGCTTGTGTGAGCCCCGGAGAGAAACTCCAAAACAATCT  1440

Qy  1441  GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500

Qy  1501  TCTATATTTAAGTGTGTGTGTATTCCATGTGTATTGTGAGTGTGTGTGTGTA  1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  TCTATATTTAAGTGTGTGTGTATTCCATGTGTATTGTGAGTGTGTGTGTGTA  1560

Qy  1561  TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA  1620

Qy  1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGGAATCTTTGAAGGGACTCAAACCT  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGGAATCTTTGAAGGGACTCAAACCT  1680

Qy  1681  TTACAAGAAAGGATGTGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  TTACAAGAAAGGATGTGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy  1741  GAACCACTGTGTTGTCTGTGAGCTTTCTGTTGTTTCCTGGGAGGGGGTGGGTCAGTGGG  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GAACCACTGTGTTGTCTGTGAGCTTTCTGTTGTTTCCTGGGAGGGGGTGGGTCAGTGGG  1800

Qy  1801  GAAAGGGGCATTAAGATGTTATTGGAACCCTTTCGTGTCTTTCTGTTTTTCTAA  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GAAAGGGGCATTAAGATGTTATTGGAACCCTTTCGTGTCTTTCTGTTTTTCTAA  1860

Qy  1861  AATTCACAGGGAAGCTTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  AATTCACAGGGAAGCTTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920

Qy  1921  AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA  1980

Qy  1981  CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAATCAACTTTGTGGGTGGAGTTC  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAATCAACTTTGTGGGTGGAGTTC  2040

Qy  2041  TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGTTC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGTTC  2100

Qy  2101  TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCCATGTGTAGGTAGAACATTTCTTAAT  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCCATGTGTAGGTAGAACATTTCTTAAT  2160

Qy  2161  GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCGTATAGCTAAAGTTTTTCTTGTA  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCGTATAGCTAAAGTTTTTCTTGTA  2220

Qy  2221  CATGAAACCCTGGAAGACTACTACAAAAAAACTGTTGTTTGGCCCCCATGCAGGTGAA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CATGAAACCCTGGAAGACTACTACAAAAAAACTGTTGTTTGGCCCCCATGCAGGTGAA  2280

Qy  2281  CTCATTTGTGCTTTAATAGAAAAGACAAATCCACCCAGTAATATTGCCCTTACGTAGT  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CTCATTTGTGCTTTAATAGAAAAGACAAATCCACCCAGTAATATTGCCCTTACGTAGT  2340

Qy  2341  TGTTTACCATTATTCAAAGCTCAAAGATTTGAAGCCCCTCACAAAATCTGTGATT  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  TGTTTACCATTATTCAAAGCTCAAAGATTTGAAGCCCCTCACAAAATCTGTGATT  2400

Qy  2401  AATTTGCTTAATTAGAGCTTCTCATCCCTCACCTACCATAAAACCAGCCATATTA  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  AATTTGCTTAATTAGAGCTTCTCATCCCTCACCTACCATAAAACCAGCCATATTA  2460
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Qy  361  ACGAACCTGGGCTCCTGAACAGCATGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  ACGAACCTGGGCTCCTGAACAGCATGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420

Qy  421  AGTCCCTATAACACAGACACACGGCCAGAACAGCGTCACGGCCGCCCTCGCCCTACGCACAG  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  AGTCCCTATAACACAGACACACGGCCAGAACAGCGTCACGGCCGCCCTCGCCCTACGCACAG  480

Qy  481  CCCAGTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCTCCAACACCGACTAC  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  CCCAGTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCTCCAACACCGACTAC  540

Qy  541  CCAGGCCCGCACAGTTTCGACGTGTCCTTCCAGCAGTGCGAGCACCGCCAGTCGGCCACC  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  CCAGGCCCGCACAGTTTCGACGTGTCCTTCCAGCAGTGCGAGCACCGCCAGTCGGCCACC  600

Qy  601  TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC  660

Qy  661  CAGATCAAGGTGATGACACCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  CAGATCAAGGTGATGACACCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTAC  720

Qy  721  AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCCGTGCCCAACCATGAGCTGAGCCGT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCCGTGCCCAACCATGAGCTGAGCCGT  780

Qy  781  GAATTCAACGACAGAGGGACAGAGATGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGACAGC  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GAATTCAACGACAGAGGGACAGAGATGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGACAGC  840

Qy  841  CATGCCCAGTATGTAGAAGATCCATCACAGGAAGACAGAGTGTCGGTACCTTATGAG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  CATGCCCAGTATGTAGAAGATCCATCACAGGAAGACAGAGTGTCGGTACCTTATGAG  900

Qy  901  CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960

Qy  961  TGTGTTGGAGGGGATGAACACCCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT  1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  TGTGTTGGAGGGGATGAACACCCGCCGTCCAATTTTAATCATTGTTACTCTGGAAACCAGAGAT  1020

Qy  1021 GGGCAAGTCCTGGGCCGACGCGTCTTTGAGGCCCGGATCTGCTGCTCGTCGCTTGCCCAGGAGGAC  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGGCAAGTCCTGGGCCGACGCGTCTTTGAGGCCCGGATCTGCTGCTCGTCGCTTGCCCAGGAGGAC  1080

Qy  1081 AGGAAGGCGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGT  1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGGAAGGCGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGT  1140

Qy  1141 GATGGTACGGAACGCGCCGTTCGTCAGAACCTGTATACTTACCAGTGATGACATATCCATCAAG  1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GATGGTACGGAACGCGCCGTTCGTCAGAACCTGTATACTTACCAGTGATGACATATCCATCAAG  1200

Qy  1201 AAACGAAGATCCCCAGATGTTGAAGATCAAAGATCATGCAGTACCTTCCTCAGACACTTAT  1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AAACGAAGATCCCCAGATGTTGAAGATCAAAGATCATGCAGTACCTTCCTCAGACACTTAT  1260

Qy  1261 GAAATGCTGTTGAAGATCAAAGATCAAAGAGTCCCTGGAACTCAGCAGTACCTTCCTCAGCACACA  1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GAAATGCTGTTGAAGATCAAAGATCAAAGAGTCCCTGGAACTCAGCAGTACCTTCCTCAGCACACA  1320

Qy  1321 ATTGAAACGTACAGGCAACAGCAACAGCGCACGCACACTTACTTCAGAAACATCTC  1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATTGAAACGTACAGGCAACAGCAACAGCGCACGCACACTTACTTCAGAAACATCTC  1380

Qy  1381 CTTTCAGCCTGCTTCAGGAATGCAGTTGTGAGCCGGAGAAACTCCAAAACAATCT  1440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTTTCAGCCTGCTTCAGGAATGCAGTTGTGAGCCGGAGAAACTCCAAAACAATCT  1440

Qy  1441 GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCATAGAGCCCTATC  1500

Qy  1501 TCTATATTTAAGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTA  1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TCTATATTTAAGTGTGTGTGTATTCCATGTGTATATGTGAGTGTGTGTGTGTA  1560

Qy  1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAACACTTTGGCTCAGAGA  1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTGAAACACTTTGGCTCAGAGA  1620

Qy  1621 CCCAACTGCTCAAAGGCACAAAGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGACTCAAACCT  1680
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CCCAACTGCTCAAAGGCACAAAGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGACTCAAACCT  1680

Qy  1681 TTACAAGAAAGGATGTTTTCTGCAGATTTGTATCCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TTACAAGAAAGGATGTTTTCTGCAGATTTGTATCCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy  1741 GAACCACTGTGTTTGTCTGTGGAGCTTTCTGTTCTGTCTTCCTGGGAGGAGGGGTCAGGTGGG  1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GAACCACTGTGTTTGTCTGTGGAGCTTTCTGTTCTGTCTTCCTGGGAGGAGGGGTCAGGTGGG  1800

Qy  1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTTCTGTTTCTGTGTTTCTAA  1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTTCTGTTTCTGTGTTTCTAA  1860

Qy  1861 AATTCACAGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AATTCACAGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG  1920

Qy  1921 AAAAAAGTTGTTATTGTCGTGCATAAGTAAGTGTAGGTGACTCAGTCAGA  1980
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 AAAAAAGTTGTTATTGTCGTGCATAAGTAAGTGTAGGTGACTCAGTCAGA  1980

Qy  1981 CCCTTTTAATGCTGGCAGCGAGTGATCATGTAATAATAATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC  2040
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CCCTTTTAATGCTGGCAGCGAGTGATCATGTAATAATAATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC  2040

Qy  2041 TACTGCTGGGCAGCGAGTGATCATTATTGTGTCTCCCCTCATGTGTAGGTAGAACATTTCTTAAT  2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TACTGCTGGGCAGCGAGTGATCATTATTGTGTCTCCCCTCATGTGTAGGTAGAACATTTCTTAAT  2100

Qy  2101 TTTGTGAGAACTTGCATTATTATTGTCTGTATGTTGGGATCTGTTATGCTAAAGTTTTTCTTGTA  2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TTTGTGAGAACTTGCATTATTATTGTCTGTATGTTGGGATCTGTTATGCTAAAGTTTTTCTTGTA  2160

Qy  2161 GCTGTGTACCTGCCTCTGCCACTGTGGGATCGTCGTTATGCTCAGCAGGTGAA  2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCTGTGTACCTGCCTCTGCCACTGTGGGATCGTCGTTATGCTCAGCAGGTGAA  2220

Qy  2221 CATGAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTTGTTTGGCCCCCAGTAATATTGCCCTTACGTAGT  2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATGAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTTGTTTGGCCCCCAGTAATATTGCCCTTACGTAGT  2280

Qy  2281 CTCATTTGTGTCTTTAATGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTCATTTGTGTCTTTAATGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340

Qy  2341 TGTTTACCATTATTCAAAGCTCAAAAATAGAATTGAAGCCCTCCACAAAATCTGTGATT  2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGTTTACCATTATTCAAAGCTCAAAAATAGAATTGAAGCCCTCCACAAAATCTGTGATT  2400

Qy  2401 AATTTGCTTAATTAGAGCTTCATCCCTACCAGCTAAAAACCAGCCATATTA  2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AATTTGCTTAATTAGAGCTTCATCCCTACCAGCTAAAAACCAGCCATATTA  2460

Qy  2461 CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTGAGTAAGGAGATCCAAGC  2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTGAGTAAGGAGATCCAAGC  2520

Qy  2521 AGACGTGTTAAAATCAGCACTCCTGACTGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT  2580
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RESULT 12
US-10-393-567-64
; Sequence 64, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-64

Query Match   100.0%;   Score 2816;   DB 16;   Length 2816;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 2816;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

[Nucleotide sequence alignment between Query (Qy) and Database (Db) sequences; 100% identity over positions 1–2816 and continuing blocks 421–2816.]

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Qy  2641 TTAAGATAATAGCAGCATAAAGACTTTAAAAATGTTCCTCCCCCCATCTTCCACACCCAGT 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTAAGATAATAGCAGCATAAAGACTTTAAAAATGTTCCTCCCCCCATCTTCCACACCCAGT 2700

Qy  2701 CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTGTTATTGAGGCTGTTGCTT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CACCAGCACTGTATTTCTGTCACCAAGACAATGATTTCTGTTATTGAGGCTGTTGCTT 2760

Qy  2761 TTGTGGATGTGTGATTTAATTTTCAATAAACTTTGCATCTTGGTTGTTAAAAGAAA 2816
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TTGTGGATGTGTGATTTAATTTTCAATAAACTTTGCATCTTGGTTGTTAAAAGAAA 2816
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RESULT 13
US-10-393-567-65
; Sequence 65, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-65

Query Match   100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAAATTTGAAACTTCACGGTGTGCCACCCT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAAATTTGAAACTTCACGGTGTGCCACCCT 60

Qy   61 ACAGTACTGCCCTGACCCTTACATCGCAGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACAGTACTGCCCTGACCCTTACATCGCAGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120

Qy  121 AAAGAAAGTTATTACCGATCGACCATGTCCCAGAGCACACAGACACAGAATTCCTCAGT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 AAAGAAAGTTATTACCGATCGACCATGTCCCAGAGCACACAGACACAGAATTCCTCAGT 180

Qy  181 CCAGAGGTTTCAGCATATCTGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCAGAGGTTTCAGCATATCTGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC 240

Qy  241 ATTGACTTGACTTGTGGATGAACCATCAGAAGATGTGGCACAAGATTGAGATT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 ATTGACTTGACTTGTGGATGAACCATCAGAAGATGTGGCACAAGATTGAGATT 300

Qy  301 AGCATGGACTGTATCCGCAGGACTCGAGGACCCTGAGTGACCTCGAGGACCCACAGTAC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AGCATGGACTGTATCCGCAGGACTCGAGGACCCTGAGTGACCTCGAGGACCCACAGTAC 360

Qy  361 ACGAACCTGGGCTCCTGAACAGGTCATGGACCAGGATTCAGAACGGCTCCTCGTCCACC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 ACGAACCTGGGCTCCTGAACAGGTCATGGACCAGGATTCAGAACGGCTCCTCGTCCACC 420

Qy  421 AGTCCCTATAACAGACCACGAGCCGCAGAACGCGTCCTCGCCCTACGCACAG 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AGTCCCTATAACAGACCACGAGCCGCAGAACGCGTCCTCGCCCTACGCACAG 480

Qy  481 CCCAGCTTCCACCTTCGATGCTCTCTCCTCCATCCCCTCAACACCGACTAC 540
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Db  481 CCCAGCTTCCACCTTCGATGCTCTCTCCTCCATCCCCTCAACACCGACTAC 540
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Qy  1561 TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAGACACTTGGCTCAGAGA 1620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAGACACTTGGCTCAGAGA 1620

Qy  1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACCT 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTGAAGGGACTCAAACCT 1680

Qy  1681 TTACAAGAAAGGATGTGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TTACAAGAAAGGATGTGTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG 1740

Qy  1741 GAACCACTGTGTTTGTCTGTGAGCTTTCTGTTCCTGGGAGGGAGGGGTCAGGTGGG 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GAACCACTGTGTTTGTCTGTGAGCTTTCTGTTCCTGGGAGGGAGGGGTCAGGTGGG 1800

Qy  1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTCTTCCTTCTGTTGTTTTCTAA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTCTTCCTTCTGTTGTTTTCTAA 1860

Qy  1861 AATTCACAGGAGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AATTCACAGGAGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920

Qy  1921 AAAAAGTTGTTATTGTCGTGCATAAGTAAGTGTAGGTGACTCAGTCAGA 1980
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 AAAAAGTTGTTATTGTCGTGCATAAGTAAGTGTAGGTGACTCAGTCAGA 1980

Qy  1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGGTGTCAAGTG 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGGTGTCAAGTG 2040

Qy  2041 TACTGCTGGGCAGCGAGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGTTC 2100
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Db  2041 TACTGCTGGGCAGCGAGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGTTC 2100

Qy  2101 TTTGTGAGAACTTGCATTATTGTGTCCTCCCCATGTGTAGGTAGAACATTTCTTAAT 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 TTTGTGAGAACTTGCATTATTGTGTCCTCCCCATGTGTAGGTAGAACATTTCTTAAT 2160

Qy  2161 GCTGTGTACCTGCCTGCCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCCTGTA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCTGTGTACCTGCCTGCCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCCTGTA 2220

Qy  2221 CATGAAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATGAAAACCCTGGAAGACCTACTACACAAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280

Qy  2281 CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy  2341 TGTTTACCATTATTCAAAGCTCAAAGCTCAAATAGAATTGAAGCCCTCTCCACAAAATCTGTGATT 2400
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Db  2341 TGTTTACCATTATTCAAAGCTCAAAGCTCAAATAGAATTGAAGCCCTCTCCACAAAATCTGTGATT 2400

Qy  2401 AATTTGCTTAATTAGAGCACTCTATCCCTCAAGCCTACCTACCAGCCATATTA 2460
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Db  2401 AATTTGCTTAATTAGAGCACTCTATCCCTCAAGCCTACCTACCAGCCATATTA 2460

Qy  2461 CTGATACTGTTCAGTGCATTTGAGTGACTTACGTTTTGAGTAAGTGAGATCCAAGC 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTGATACTGTTCAGTGCATTTGAGTGACTTACGTTTTGAGTAAGTGAGATCCAAGC 2520

Qy  2521 AGAGACGTGTAAAATCAGCACTCCTGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 AGAGACGTGTAAAATCAGCACTCCTGACTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy  2581 TTCTTTTTTTTTACTCAAAAGTTTAGAGAATCTCGTTTCTTTCCATTTTAAAAACATATT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TTCTTTTTTTTTACTCAAAAGTTTAGAGAATCTCGTTTCTTTCCATTTTAAAAACATATT 2640
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Left column:

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Qy    541  CCAGGCCGCACAGTTCGACGTGTCTTCAGCAGTCGAGCACCGCCAGTCGGCCACC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCAGGCCGCACAGTTCGACGTGTCTTCAGCAGTCGAGCACCGCCAGTCGGCCACC  600

Qy    601  TGGACGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC  660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TGGACCGTATTCCACTGAACTGAAGAAACTCTACTGCCAAATTGCAAAGACATGCCCCATC  660

Qy    661  CAGATCAAGGTGATGACCGAGCGCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGCTCTAC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CAGATCAAGGTGATGACCGAGCGCCCACCTCCTCAGGGAGCTGTTATCCGCGCCATGCCTGCTCTAC  720

Qy    721  AAAAAAGCTGAGCACCTCACCGAGGTGGTGAAGCCGTGCCCCAACCATGAGCTGAGCCGT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AAAAAAGCTGAGCACCTCACCGAGGTGGTGAAGCCGTGCCCCAACCATGAGCTGAGCCGT  780

Qy    781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGAACAGC  840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGC  840

Qy    841  CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTCGTCTGGTACCTTATGAG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CATGCCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTCGTCTGGTACCTTATGAG  900

Qy    901  CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT  960

Qy    961  TGTGTTGGAGGGATGAACCGCCTCGTTGAGGGCCCGACCTGCTTGAGGCCCCGGATCTTC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TGTGTTGGAGGGATGAACCGCCTCGTTGAGGGCCCGACCTGCTTGAGGCCCCGGATCTTC  1020

Qy   1021  GGGCAAGTCCTGGGCCGTTCGTCAGACAACACACAGGTATCCAGATGACATCCATCAAG  1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGGCAAGTCCTGGGCCGTTCGTCAGACAACACACAGGTATCCAGATGACATCCATCAAG  1080

Qy   1081  AGGAAGGCGGATGAAGAATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACCTTCCTCAGCACACA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  AGGAAGGCGGATGAAGAATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACCTTCCTCAGCACACA  1140

Qy   1141  GATGGTACGGAAGCGCCCGTTTCGTCAGAACAACAGCAGCACACAGTGGTATCCAGATGACATCCATCAAG  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GATGGTACGGAAGCGCCCGTTTCGTCAGAACAACAGCAGCACACAGTGGTATCCAGATGACATCCATCAAG  1200

Qy   1201  AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTTAT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AAACGAAGATCCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTTAT  1260

Qy   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGACTACCTTCCTCAGCACACA  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCATGCGACTACCTTCCTCAGCACACA  1320

Qy   1321  ATTGAAACGTACAGGCAACAGCACCAGCACACTTACTTCAGAAAACATCTC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  ATTGAAACGTACAGGCAACAGCACCAGCACACTTACTTCAGAAAACATCTC  1380

Qy   1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTTGGAGCCCCGGAGAATCTCCAAAACAATCT  1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CTTTCAGCCTGCTTCAGGAATGAGCTTGTTGGAGCCCCGGAGAATCTCCAAAACAATCT  1440

Qy   1441  GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCCATAGAGCCCTATC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  GACGTCTTCTTTAGACATTCCAAGCCCCCAAACCGATCAGTGTACCCCATAGAGCCCTATC  1500

Qy   1501  TCTATATTTTAAGTGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGTGTA  1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  TCTATATTTTAAGTGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGTGTA  1560

Qy   1561  TGTGTGTGCGTGTGTATCAGCCCTCATAAACAGACTTGAAGACACTTGGCTCAGAGA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  TGTGTGTGCGTGTGTATCAGCCCTCATAAACAGACTTGAAGACACTTGGCTCAGAGA  1620

Qy   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGGACTCAAACCT  1680
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Right column:

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Db   1621  CCCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGGACTCAAACCT  1680

Qy   1681  TTACAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TTACAGAAAGGATGTTTTCTGCAGATTTGTATCCTTAGACCGGCCATTGGTGGGTGAG  1740

Qy   1741  GAACCACTGTGTTGTCGTGTGAGCTTTCTGTGTTCCTGGAGAGTGGGAGGGGTCAGGTGGG  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  GAACCACTGTGTTGTCGTGTGAGCTTTCTGTGTTCCTGGAGAGTGGGAGGGGTCAGGTGGG  1800

Qy   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTCTTCTCGTGTTTTCTAA  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  GAAAGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTCTTCTCGTGTTTTCTAA  1860

Qy   1861  AATTCACAGGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  AATTCACAGGGAAGCTTTGAGCAGGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG  1920

Qy   1921  AAAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTAGTGTAGGTGTCAAGTG  1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  AAAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTAGTGTAGGTGTCAAGTG  1980

Qy   1981  CCCTTTTAATGCTGTGGTCATGTAATAATATATTGCAAGTAATAATATTGCAAGTTC  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CCCTTTTAATGCTGTGGTCATGTAATAATATATTGCAAGTAATAATATTGCAAGTTC  2040

Qy   2041  TACTGCTGGGCAGCGAGGTGATCATTACCAAAAGTAATCAACTTTGTGGGTGGAGGTTC  2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  TACTGCTGGGCAGCGAGGTGATCATTACCAAAAAGTAATCAACTTTGTGGGTGGAGGTTC  2100

Qy   2101  TTTGTGAGAACTTGCATTATTTGTGTCCTCCCTACATGTGTAGGTAGAAACATTTCTTAAT  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TTTGTGAGAACTTGCATTATTTGTGTCCTCCCTACATGTGTAGGTAGAACATTTCTTAAT  2160

Qy   2161  GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCTGTGTACCTGCCTCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA  2220

Qy   2221  CATGAAACCCTGGAAGACCTGGAAGACCTACTACAAAAAAACTGTGTTTGGCCCCATAGCAGTGAA  2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CATGAAACCCTGGAAGACCTGGAAGACCTACTACAAAAAAACTGTGTTTGGCCCCATAGCAGGTGAA  2280

Qy   2281  CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT  2340

Qy   2341  TGTTTACCATTATTCAAAGCTCAAAAGTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  TGTTTACCATTATTCAAAGCTCAAAAGTCAAAATAGAATTTGAAGCCCTCTCACAAAATCTGTGATT  2400

Qy   2401  AATTTGCTTAATTAGAGCTTCTATCCCTCAGCTCTACTTACTTCAGAAAACCAGCCATATTA  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  AATTTGCTTAATTAGAGCTTCTATCCCTCAGCTCTACTTACTTCAGAAAACCAGCCATATTA  2460

Qy   2461  CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC  2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  CTGATACTGTTCAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC  2520

Qy   2521  AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTTT  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTGAAAGGGTAGACTACTTT  2580

Qy   2581  TTCTTTTTTTTTACTTCAAAAGTTAGAGAATCTCTGTTTCTTCCCCTCCATTTTAAAAACATATT  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TTCTTTTTTTTTTTACTTCAAAAGTTAGAGAATCTCTGTTTCTTCCATTTTAAAAACATATT  2640

Qy   2641  TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCTCCATCTTCCCACACCCAGT  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCTCCCCCTCCATCTTCCCACACCCAGT  2700

Qy   2701  CACCGACACTGTATTTTCTGTCACCAAGACAATGAATTGATTTCGTGTTATTGGAGGCTGTTGCTT  2760
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Db  2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGATTTCTTGTTATTGAGGCTGTGTGCTT 2760
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Qy  2761 TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA 2816
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Db  2761 TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTGGTTTAAAAGAAA 2816

RESULT 14
US-10-394-087-26
; Sequence 26, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-394-087-26

Query Match             100.0%;  Score 2816;  DB 16;  Length 2816;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  2816;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT   60
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Db     1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT   60

Qy    61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ACAGTACTGCCCTGACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG  120

Qy   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGAGCAAATGAATTCCTCAGT  180
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Db   121 AAAGAAAGTTATTACCGATCCACCATGTCCCAGAGCACACAGAGCAAATGAATTCCTCAGT  180

Qy   181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCC  240

Qy   241 ATTGAACTTGAACTTTGTGGATGAACCATCAGAAGAGATGGTGCGACAAACAAGATTGAGATT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTGAACTTGAACTTTGTGGATGAACCATCAGAAGAGATGGTGCGACAAACAAGATTGAGATT  300

Qy   301 AGCATGGACTGTATCCGACTCGGACTCGGACTGAGTGGCCACCAGTAC  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGCATGGACTGTATCCGACTCGGACTCGGACTGAGTGTGGCCACCAGTAC  360

Qy   361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGAACCTGGGGCTCCTGAACAGCATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACC  420

Qy   421 AGTCCCTATAACACAGACCACGCGCAGAACACCGCAGCGCGTCACGGCGCCCTCGCCCTACGGCACAG  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGTCCCTATAACACAGACCACGCGCAGAACACCGCAGCGCGTCACGGCGCCCTCGCCCTACGGCACAG  480

Qy   481 CCCAGCTCACCTTCGATGCTCTCTCCATCCCGCCATCCCCGCCATCCCCGCCAGTAC  540
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Db   481 CCCAGCTCACCTTCGATGCTCTCTCCATCCCGCCATCCCCGCCATCCCCGCCAGTAC  540

Qy   541 CCAGGCCCGCCACAGTTCGACGTGTCCTTCCAGCAGTCAGCAGTCGGCACCGGCACC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCAGGCCCGCACAGTTCGACGTGTCCTTCCAGCAGTCAGCAGTCGGCACCGGCACC  600

Qy   601 TGGACGTATTCCACTGAACTGAAGAGAAACTCTACTGCCCAAATTGCAAAGACATGCCCCATC  660
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Db   601 TGGACGTATTCCACTGAACTGAAGAGAAACTCTACTGCCCAAATTGCAAAGACATGCCCCATC  660
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Db 601 TGGACGTATTCCACTGAACTGAAGAGAAACTCTACTGCCCAAATTGCAAAGACATGCCCCATC 660

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Qy   661 CAGATCAAGGTGATGACCCACCTTCCTCAGGAGCTGTATCCGCGGCCATGCGCCATGCGCCTAC  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGATCAAGGTGATGACCCACCTTCCTCAGGAGCTGTATCCGCGGCCATGCGCCATGCGCCTAC  720

Qy   721 AAAAAAGCTGAGCACGTCACGGAGCGGTGAGCGGTGCCCCAACCATGAGCTGAGCCGT  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAAAAAGCTGAGCACGTCACGGAGCGGTGAGCGGTGCCCCAACCATGAGCTGAGCCGT  780

Qy   781 GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCGAGTAGAGGGAACAGC  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAATTCAACGAGGGACAGATTGCCCCTCCTAGTCATTGATTCGAGTAGAGGGAACAGC  840

Qy   841 CATGCCCAGTATGTAGAAGATCCCATCACAGAAGACACAGTCTTGTACACAATTTCATTGTAACAGCAGT  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CATGCCCAGTATGTAGAAGATCCCATCACAGAAGACACAGTCTTGTACACAATTTCATTGTAACAGCAGT  900

Qy   901 CCACCCCAGGTTGGCACTGAATTCACGACACGTCCAATTTTAATCATTGTACTCTGGAAACCAGCAGAT 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCACCCCAGGTTGGCACTGAATTCACGACACGTCCAATTTTAATCATTGTACTCTGGAAACCAGCAGAT 1020

Qy   961 TGTGTTGGAGGGATGAACCGCGTCCAATTTGAGGCCCGATCTGCTTTGAGGCCCAGGAAGAGAC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGTGTTGGAGGGATGAACCGCGTCCAATTTTAATCATTGTACTCTGGAAACCAGCAGAT 1020

Qy  1021 GGGCAAGTCCTGGGCCGAGCGTGCTTTGAGGCCCGATCTGCTTTGAGGCCCGATCTGCTTTGCCACAGTACAAAGAACGGT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGGCAAGTCCTGGGCCGAGCGTGCTTTGAGGCCCGATCTGCTTTGAGGCCCGATCTGCTTTGCCACAGTACAAAGAACGGT 1140

Qy  1081 AGGAAGGCGGATGAAGATAGCATCAGAAGCAGCAAGTTCGGACAGTGCATCCATCAAG 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGGAAGGCCGATGAAGATAGCATCAGAAGCAGCAAGTTCGGACAGTGCATCCATCAAG 1140

Qy  1141 GATGGTACGAGAGCGCCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GATGGTACGAGAGCGCCCGTTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200

Qy  1201 AAACGAAGATCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AAACGAAGATCCCAGATGATGAACTGTTATACTTACCAGTGAGGGGCCGTGAGACTTAT 1260

Qy  1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCAGTACCTTCCTCAGCACACA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GAAATGCTGTTGAAGATCAAAGAGTCCCTGGAACTCAGTACCTTCCTCAGCACACA 1320

Qy  1321 ATTGAAACGTACAGGCAACATCAGAACAGATGGTGCGACAAACAAGATTGAGATGATCTCTC 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 ATTGAAACGTACAGGCAACATCAGAACAGATGGTGCGACAAACAAGATTGAGATGATCTCTC 1380

Qy  1381 CTTTCAGCCTGCTTGCTTCGGAATGAGCTTGTGTGGAGCCCCGGAGAAACTCCAAAACAATCT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CTTTCAGCCTGCTTGCTTCGGAATGAGCTTGTGTGGAGCCCCGGAGAAACTCCAAAACAATCT 1440

Qy  1441 GACGTCTTCTTTAGACATTCAAGCCCCCAAACCGATCAGTGTACCCCATAGAGACCCTATC 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 GACGTCTTCTTTAGACATTCAAGCCCCCAAACCGATCAGTGTACCCCATAGAGACCCTATC 1500

Qy  1501 TCTATATTTTAAGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TCTATATTTTAAGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTA 1560

Qy  1561 TGTGTGTGCGTGTGTATCTAGCCCTCATAAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 TGTGTGTGCGTGTGTATCTAGCCCTCATAAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620

Qy  1621 CCCAACTGCTCAAAGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAAACCT 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CCCAACTGCTCAAAGCACAAAGCCACTAGTGAGAGAATCTTTTGAAGGGACTCAAAACCT 1680

Qy  1681 TTACAAGAAAGGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGGTGGGTGAG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 TTACAAGAAAGGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGGTGGGTGAG 1740
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RESULT 15
US-10-394-087-27
; Sequence 27, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-394-087-27

Query Match   100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TCGTTGATATCAAAGACAGTTGAAGGAAATGAATTTGAAACTTCACGGTGTGCCACCCT 60

Qy   61 ACAGTACTGCCCTGCACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACAGTACTGCCCTGCACCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120

Qy   121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGAGACAAATGAATTCCTCAGT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGAGACAAATGAATTCCTCAGT 180

Qy   181 CCAGAGGTTTCCAGCATTCTGGATTTTCTGGAATTCTGGAACAGCCTATATGTTCAGTCAGCCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAGAGGTTTCCAGCATTCTGGATTTTCTGGAATTCTGGAACAGCCTATATGTTCAGTCAGCCC 240

Qy   241 ATTGACTTGAACTTGTGATGATGACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTGACTTGAACTTGTGATGATGACCATCAGAAGATGGTGCGACAAACAAGATTGAGATT 300

Qy   301 AGCATGGACTGTATCCGCATGCAGAGCTCGGACTCGGACTCGAGTGACCTGAGTGCCACAGTAC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGCATGGACTGTATCCGCATGCAGAGCTCGGACTCGGACTCGAGTGACCTGAGTGCCACAGTAC 360

Qy   361 ACGAACCTGGGGCTCCTGAACAGCAGACCAGCAGATTCAGAAGGCTCGTCGTCCACC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGAACCTGGGGCTCCTGAACAGCAGACCAGCAGATTCAGAAGGCTCGTCGTCCACC 420

Qy   421 AGTCCCTATAACACAGACAGCGCGCAGAACAGCGTCACCGGCGCCCTCGCCCTCCAACACCGACTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGTCCCTATAACACAGACAGCGCGCAGAACAGCGTCACCGGCGCCCTCGCCCTCCAACACCGACTAC 480

Qy   481 CCCAGCTCCACCTTCGATGCTCTCTCTCTCCAACGTCCTTCCAGCAGTGTCCTTCCAGACGTCGGGCACC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CCCAGCTCCACCTTCGATGCTCTCTCTCTCCAACGTCCTTCCAGCAGTGTCCTTCCAGACGTCGGGCACC 540

Qy   541 CCAGGCCCGCACAGTTCGACGTGCCTTCCTCCAGCAGTCGAGCAGTCGAGCAGTCGGGCACC 600
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Db   541 CCAGGCCCGCACAGTTCGACGTGCCTTCCTCCAGCAGTCGAGCAGTCGAGCAGTCGGGCACC 600

Qy   601 TGGACGTATTCCACTGGAATCTGAAGAAACTTCACTGCCAAATTGCAAAGACATGCCCCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGGACGTATTCCACTGGAATCTGAAGAAACTTCACTGCCAAATTGCAAAGACATGCCCCATC 660

Qy   661 CAGATCAAGGTGATGACCCCACCTTCCACCTCCAGGGAGCTGTTATCCGCGGCAGTGTTATCCGCGGCAGTGTCTGCTCTAC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGATCAAGGTGATGACCCCACCTTCCACCTCCAGGGAGCTGTTATCCGCGGCAGTGTCTGCTCTAC 720

Qy   1741 GAACCACTGTGTTGTCTGTGAGCTTTCGTGTTGTTCCTGGGACGGAGGAGGGTCAGGTGGG 1800
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Db   1741 GAACCACTGTGTTGTCTGTGAGCTTTCGTGTTGTTCCTGGGACGGAGGAGGGTCAGGTGGG 1800

Qy   1801 GAAAGGGGCATTAAGATGTTATTGGAACCCTTTCGTCTTCTTCGTCTTCTTCGTGTTTTTCTAA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAAAGGGGCATTAAGATGTTATTGGAACCCTTTCGTCTTCTTCGTCTTCTTCGTGTTTTTCTAA 1860

Qy   1861 AATTCACAGGGAAGCTTTTGAGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AATTCACAGGGAAGCTTTTGAGCAGTCTCAAACTTAAGATGTCTTTTTAAGAAAAGGAG 1920

Qy   1921 AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA 1980
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Db   1921 AAAAAGTTGTTATTGTCTGTGCATAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA 1980

Qy   1981 CCCTTTAATGCTGTCATGTAATAATATTGCAAGTAGTAAGAAACGAGAGGTGTCAAGTG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CCCTTTAATGCTGTCATGTAATAATATTGCAAGTAGTAAGAAACGAGAGGTGTCAAGTG 2040

Qy   2041 TACTGCTGGGCAGCGAGGTGATCATTACCAAAGTAATCAACTTTGTGGGTGGAGAGTTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TACTGCTGGGCAGCGAGGTGATCATTACCAAAGTAATCAACTTTGTGGGTGGAGAGTTC 2100

Qy   2101 TTTGTGAGAACTTGCATTATTGTGTCCTCCCCCATGTGTAGGTAGGTAGAACATTTCTTAAT 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TTTGTGAGAACTTGCATTATTGTGTCCTCCCCCATGTGTAGGTAGGTAGAACATTTCTTAAT 2160

Qy   2161 GCTGTGTACCTGCCTCGCCCTCCGCCACTGTGTATGGCATCGTATGTGTAAAGTTTTTCTTGTA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCTGTGTACCTGCCTCGCCCTCCGCCACTGTGTATGGCATCGTATGTGTAAAGTTTTTCTTGTA 2220

Qy   2221 CATGAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTTGGCCCCCATAGCAGTGA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATGAAACCCTGGAAGACCTACTACAAAAAAACTGTTGTTTGGCCCCCATAGCAGTGA 2280

Qy   2281 CTCATTTGTGCTTTAATAGAAAGACAAATCACCCCAGTAATATTGCCCTTACGTAGT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CTCATTTGTGCTTTAATAGAAAGACAAATCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy   2341 TGTTACCATTATTCAAAGCTCAAAGCTCAAAATGAATTTGAAGCCCTCCACAAAATCTGTGATT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGTTACCATTATTCAAAGCTCAAAGCTCAAAATGAATTTGAAGCCCTCCACAAAATCTGTGATT 2400

Qy   2401 AATTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAAACCAGCCATATTA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 AATTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAAACCAGCCATATTA 2460

Qy   2461 CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTGATACTGTTCAGTGCATTAGCCAGGAGACTTACGTTTGAGTAAGTGAGATCCAAGC 2520

Qy   2521 AGAGCGTGTTAAAATCAGCACTCCTGGACTTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AGAGCGTGTTAAAATCAGCACTCCTGGACTTGGAAATTAAAGATTGAAAGGGTAGACTACTT 2580

Qy   2581 TTCTTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTCTTTCTTCTTCATTTTAAAAACATATT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTCTTTTTTTTACTCAAAAGTTTAGAGAATCTCTGTTCTTTCTTCTTCATTTTAAAAACATATT 2640

Qy   2641 TTAAGATAATAGACATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCACACCCCAGT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TTAAGATAATAGACATAAAGACTTTAAAAATGTTCCTCCCCCATCTTCCCACACCCCAGT 2700

Qy   2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGACTTTCTGTATTGAGGCTGTTGCTT 2760
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Db   2701 CACCAGCACTGTATTTTCTGTCACCAAGACAATGACTTTCTGTATTGAGGCTGTTGCTT 2760

Qy   2761 TTGTGGATGTGTGATTTAATTTCAATAAACTTTGCATCTTTGCATCTTTGCATCTTGCTCTAC 2816
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Qy   721 AAAAAAGCTGAGCACGTCACGGAGGTCGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
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Db   721 AAAAAAGCTGAGCACGTCACGGAGGTCGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780

Qy   781 GAATTCAACGAGGAGGACAGATTGCCCCTCCAGTCATTGATTCGAGTAGGGGAACAGC 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAATTCAACGAGGAGGACAGATTGCCCCTCCAGTCATTGATTCGAGTAGGGGAACAGC 840

Qy   841 CATGCCCAGTATGTAGAAGATCCATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   901 CCACCCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAATTTCATGTGTAACAGCAGT 960

Qy   961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT 1020
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Db   961 TGTGTTGGAGGGATGAACCGCGTCCAATTTAATCATTGTTACTCTGGAAACCAGAGAT 1020

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Qy  1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT 1140
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Db  1081 AGGAAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTCGGACAGTACAAAGAACGGT 1140

Qy  1141 GATGGTACGGAGCGCCCGTTCGTCAGAGAACACACATGTATCCAGATGACATCCATCAAG 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GATGGTACGGAGCGCCCGTTCGTCAGAGAACACACATGTATCCAGATGACATCCATCAAG 1200

Qy  1201 AAACGAAGATCCCAGTAGATGAACTGTTATACTTACCAGTGAGGGCGTGAGACTTAT 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AAACGAAGATCCCAGTAGATGAACTGTTATACTTACCAGTGAGGGCGTGAGACTTAT 1260

Qy  1261 GAAATGCTGTTGAAGATCAAAGAGTCCTGGAGCCCCGGAGAAGTTCCTCAGCACACA 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GAAATGCTGTTGAAGATCAAAGAGTCCTGGAGCCCCGGAGAAGTTCCTCAGCACACA 1320

Qy  1321 ATTGAAACGTACAGGCAACAGCAGCAACAGCAACGCACTTACTTCAGGAAACATCTC 1380
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Db  1321 ATTGAAACGTACAGGCAACAGCAGCAACAGCAACGCACTTACTTCAGGAAACATCTC 1380

Qy  1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT 1440
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Db  1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCT 1440

Qy  1441 GACGTCTTCTTAGACATTCCAAGCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500
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Db  1561 TGTGTGTGCGGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620

Qy  1621 CCCAACTGCTCAAAGGCACAAAGCCACAAAGCTTTTGAAGGGACTCAAACCT 1680
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Qy  1741 TGTGTGTGCGGTGTGTTGTCTGTGTGTGTCTTTCCTGTGGTTCCTGGGGAGGGAGGGGTCAGGTGGG 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 TGTGTGTGCGGTGTGTTGTCTGTGTGTGTCTTTCCTGTGGTTCCTGGGGAGGGAGGGGTCAGGTGGG 1800

Qy  1801 GAAAGGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTCTTCTTTCTTGTTTTTTCTAA 1860
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Db  1801 GAAAGGGGGCATTAAGATGTTTATTGGAACCCTTTCTGTCTTCTTTCTTGTTTTTTCTAA 1860

Qy  1861 AATTCACAGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG 1920
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Db  1861 AATTCACAGGAAGCTTTGAGCAGTCTCAAACTTAAGATGTCTTTTAAGAAAAGGAG 1920

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Db  1981 CCCTTTTAATGCTGGTCATGTAATAATATTGCAAGTAGTAGTAAGAAACGAAGGTGTCAAGTG 2040

Qy  2041 TACTGCTGGGCAGCGAGCTGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 TACTGCTGGGCAGCGAGCTGGTGATCATTACCAAAAGTAATCAACTTGTGGGTGGAGAGTTC 2100

Qy  2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCCATGTGTAGGTAGGTAGAACATTCTTAAT 2160
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Db  2101 TTTGTGAGAACTTGCATTATTTGTGTCCTCCCCCATGTGTAGGTAGGTAGAACATTCTTAAT 2160

Qy  2161 GCTGTGTACCTGCCTCTGCCACTGTGTTGGCATCGTGTTATGCTAAAGTTTTTCTTGTA 2220
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Db  2161 GCTGTGTACCTGCCTCTGCCACTGTGTTGGCATCGTGTTATGCTAAAGTTTTTCTTGTA 2220

Qy  2221 CATGAAACCCTGGAAGACCTACTACACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CATGAAACCCTGGAAGACCTACTACACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280

Qy  2281 CTCATTTTGTGCTTTAATGAGAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CTCATTTTGTGCTTTAATGAGAGACAAATCCACCCCAGTAATATTGCCCTTACGTAGT 2340

Qy  2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAGCCCTACCTACCATAAATCGTGATT 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGTTTACCATTATTCAAAGCTCAAAATAGAATTTGAGCCCTACCTACCATAAATCGTGATT 2400

Qy  2401 AATTTGCTTAATTAGAGCTTCTATCCCCAAGCCTACCTACCATATTAAAAACATATT 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 AATTTGCTTAATTAGAGCTTCTATCCCCAAGCCTACCTACCATATTAAAAACATATT 2460

Qy  2461 CTGATACTGTTCAGTGCATTAGCCAGGACTTTGAGTAGTGAGTAAGGATCCAAGC 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CTGATACTGTTCAGTGCATTAGCCAGGACTTTGAGTAGTGAGTAAGGATCCAAGC 2520

Qy  2521 AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTAAAGGGTAGACTACTT 2580
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Db  2521 AGACGTGTTAAAATCAGCACTCCTGGACTGGAAATTAAAGATTAAAGGGTAGACTACTT 2580

Qy  2581 TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCGTTTCTTTCCATTTAAAAACATATT 2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TTCTTTTTTTACTCAAAAGTTTAGAGAATCTCGTTTCTTTCCATTTAAAAACATATT 2640

Qy  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCCCCTCCATCTTCCCACCCCAGT 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TTAAGATAATAGCATAAAGACTTTAAAAATGTTCCCCCTCCATCTTCCCACCCCAGT 2700

Qy  2701 CACCAGCACTGTATTTTCGTCACCAAGACAATGATTTCTTGTTATTGAGGCGTGTTGCTT 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 CACCAGCACTGTATTTTCGTCACCAAGACAATGATTTCTTGTTATTGAGGCGTGTTGCTT 2760

Qy  2761 TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTTGCATCTGGTTTAAAAGAAA 2816
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Db  2761 TTGTGGATGTGTGATTTTAATTTCAATAAACTTTTGCATCTTTGCATCTGGTTTAAAAGAAA 2816
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Search completed: October 3, 2005, 14:01:42
Job time : 2192 secs

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              GenCore version 5.1.6
        Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    October  3, 2005, 06:01:58 ; Search time 247 Seconds
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Title:         US-09-670-568C-1
Perfect score: 2383
Sequence:      1 MSQSTQTNEFLSPEVFQHIW.........PKQSDVFFRHSKPPNRSVYP 448

Scoring table: BLOSUM62
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        Ygapop  10.0 , Ygapext  0.5
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Searched:      1202784 seqs, 818118359 residues

Total number of hits satisfying chosen parameters:       2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-Q:/cgn2_1/USPTO_spool/US09670568/runat 03102005_070150_24303/app_query.fasta_1.647
-DB=Issued_Patents_NA -QFMT=fastap -SUFIX=rni -MINMATCH=0.1 -LOOPCL=0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	2383	100.0	2810	3	US-09-949-016-5447	Sequence 5447, Ap
2	2383	100.0	2816	3	US-09-643-597-333	Sequence 333, App
3	2383	100.0	2816	4	US-09-542-615A-333	Sequence 333, App
4	2383	100.0	2816	4	US-09-606-421B-333	Sequence 333, App
5	2383	100.0	2816	4	US-09-630-940B-333	Sequence 333, App
6	2185	91.7	1551	3	US-09-643-597-337	Sequence 337, App
7	2185	91.7	1551	4	US-09-542-615A-337	Sequence 337, App
8	2185	91.7	1551	4	US-09-606-421B-337	Sequence 337, App
9	2185	91.7	1551	4	US-09-630-940B-337	Sequence 337, App
10	2185	91.7	2270	3	US-09-643-597-332	Sequence 332, App
11	2185	91.7	2270	4	US-09-542-615A-332	Sequence 332, App
12	2185	91.7	2270	4	US-09-606-421B-332	Sequence 332, App

13	2185	91.7			US-09-630-940B-332	Sequence 332, App
14	2185	91.7		4	US-09-643-597-335	Sequence 335, App
15	2185	91.7		3	US-09-542-615A-335	Sequence 335, App
16	2185	91.7		4	US-09-606-421B-335	Sequence 335, App
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18	1813	76.1		4	US-09-643-597-336	Sequence 336, App
19	1813	76.1		3	US-09-542-615A-336	Sequence 336, App
20	1813	76.1		4	US-09-606-421B-336	Sequence 336, App
21	1813	76.1		4	US-09-630-940B-336	Sequence 336, App
22	1801.5	75.6		3	US-09-643-597-334	Sequence 334, App
23	1801.5	75.6		4	US-09-277-196-1	Sequence 1, Appli
24	1801.5	75.6		4	US-09-542-615A-334	Sequence 334, App
25	1801.5	75.6		4	US-09-606-421B-334	Sequence 334, App
26	1801.5	75.6		4	US-09-630-940B-334	Sequence 334, App
27	1801.5	75.6		3	US-09-643-597-331	Sequence 331, App
28	1801.5	75.6		4	US-09-542-615A-331	Sequence 331, App
29	1801.5	75.6		4	US-09-606-421B-331	Sequence 331, App
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33	1793.5	75.3		4	US-09-542-615A-151	Sequence 151, App
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36	1793.5	75.3		4	US-09-466-396A-151	Sequence 151, App
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44	724	30.4		1	US-08-796-101-168	Sequence 168, App
45	722.5	30.3		1	US-08-047-041A-13	Sequence 13, Appl

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                              ALIGNMENTS

RESULT 1
US-09-949-016-5447
; Sequence 5447, Application US/0994901 6
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE:  2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE:  2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 5447
;    LENGTH: 2810
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-5447

Alignment Scores:
Pred. No.:                  1.13e-250          Length:      2810
Score:                      2383.00            Matches:       448
Percent Similarity:         100.00%            Conservative:    0
Best Local Similarity:      100.00%            Mismatches:      0
Query Match:                100.00%            Indels:          0
DB:                             4              Gaps:            0

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Qy        1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
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Db   1226  CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGTGTTGAAGATCAAAGAG  1285
Qy    381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
Db   1286  TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCACAGCAA  1345
Qy    401  GlnGlnHisGlnHisLeuLeuGlnLysHisLeuSerAlaCysPheArgAsnGlu  420
Db   1346  CAGCAGCACCAGCACTTACTTCAGAAACATCTCCTTCAGCCTGCTTCAGGAATGAG  1405
Qy    421  LeuValGluProArgGluThrProLysGlnSerAspValPheArgHisSerLys  440
Db   1406  CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGTCTTCTTAGACATTCCAAG  1465
Qy    441  ProProAsnArgSerValTyrPro  448
Db   1466  CCCCCAAACCGATCAGTGTACCCA  1489

RESULT 2
US-09-643-597-333
; Sequence 333, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT: Fan, Liqun
;  APPLICANT: Kalos, Michael D.
;  APPLICANT: Bangur, Chaitanya S.
;  APPLICANT: Hosken, Nancy
;  APPLICANT: Fanger, Gary R.
;  APPLICANT: Li, Samuel X.
;  APPLICANT: Wang, Aijun
;  APPLICANT: Skeiky, Yasir A.W.
;  APPLICANT: Henderson, Robert A.
;  APPLICANT: McNeill, Patricia D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C11
;  CURRENT APPLICATION NUMBER: US/09/643,597
;  CURRENT FILING DATE: 2000-08-21
;  NUMBER OF SEQ ID NOS: 369
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 333
;  LENGTH: 2816
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-643-597-333

Alignment Scores:
Pred. No.:
Score:                     1.13e-250        Length:             2816
                           2383.00          Matches:            448
Percent Similarity:        100.00%          Conservative:       0
Best Local Similarity:     100.00%          Mismatches:         0
Query Match:               100.00%          Indels:             0
DB:                        3                Gaps:               0

US-09-670-568C-1 (1-448) x US-09-643-597-333 (1-2816)

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Qy     21  AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu  40
Db    205  GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  264
Qy     41  ProSerGluAspGlyAlaThrLysIleGluIleSerMetAspCysIleArgMetGln  60
Db    265  CCAATCAGAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG  324
Qy     61  AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuGlyLeuAsnSer  80
Db    325  GACTCCGGACCTGAGTGACCCCATGTGGCCACAGAGTACACGAACCTGGGGCTCCTGAACAGC  384
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Db    206  GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  265
Qy     41  ProSerGluAspGlyAlaThrLysIleGluIleSerMetAspCysIleArgMetGln  60
Db    266  CCAATCAGAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG  325
Qy     61  AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuGlyLeuAsnSer  80
Db    326  GACTCCGGACCTGAGTGACCCCATGTGGCCACAGAGTACACGAACCTGGGGCTCCTGAACAGC  385
Qy     81  MetAspGlnAsnIleGlnAsnGlyTyrSerSerProTyrAsnThrAspHisAla  100
Db    386  ATGGACCAGAATATCAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACCACCG  445
Qy    101  GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu  120
Db    446  CAGAACAGCGTCACGGCGCCCTCGCCGTACGCACAGCCCAGCTCCACCTTCGATGCTCTC  505
Qy    121  SerProSerProAlaIleProSerGlnAsnThrAspTyrProHisSerPheAspVal  140
Db    506  TCTCCATCACCCGCCATCCCTCCAACACCGACTACCCAGGCCCCACAGTTTCGACGTG  565
Qy    141  SerPheGlnSerSerThrAlaLysSerAlaThrThrTrpThrSerThrGluLeuLys  160
Db    566  TCCTTCCAGAGTCGAGCACCGCCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG  625
Qy    161  LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysLysValMetThrProPro  180
Db    626  AAACTCTACTGCCAAATTGCAAAGACAATGCCCCATCCAGATCAAGGTGATGACCCCACCT  685
Qy    181  ProGlnGlyAlaValIleGluArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
Db    686  CCTCAGGGAGCTGTTATCCGCCGGGCTATGCCTGTCTACAAAAAGCTGAGCACGTCACGGAG  745
Qy    201  ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
Db    746  GTGGTGAAGCGGTGTCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC  805
Qy    221  ProProHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro  240
Db    806  CCTCCTCAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC  865
Qy    241  IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
Db    866  ATCACAGGAAGACAGAGTGTCTGGTCACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  925
Qy    261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
Db    926  ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT  985
Qy    281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
Db    986  CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC  1045
Qy    301  PheGluAlaArgIleCysAlaCysSerProGlyArgAspArgLysAlaAspGluSerIle  320
Db   1046  TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGACAGGAAGGCGGATGAAGATAGCATC  1105
Qy    321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
Db   1106  AGAAAGCAACAGGTTTCGGACAGTACAAAGAACGGCGATGGTACGAAGCGCCCCTTTCGT  1165
Qy    341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
Db   1166  CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA  1225
Qy    361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
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RESULT 3
US-09-542-615A-333
; Sequence 333, Application US/0954261 5A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-333

Alignment Scores:
Pred. No.:   1.11e-250   Length: 2816
Score: 2383.00   Matches: 448
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 4   Gaps: 0

US-09-670-568c-1 (1-448) x US-09-542-615A-333 (1-2816)

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Db   145  ATGTCCCAGACGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  204

Qy    21  AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu   40
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Db   205  GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  264

Qy    41  ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265  CCATCAGAAGATGGTGCAACAAACAGATTGAGATTAGCATGGACTGTATCCGCATGCAG  324

Qy    61  AspSerAspLeuSerAspProMetTrpProGlnThrThrAsnLeuGlyLeuLeuAsnSer   80
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Db   325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACCACGAACCTGGGGCTCCTGAACAGC  384

Qy    81  MetAspGlnIleLeuGlnAsnGlySerSerSerProTyrAsnThrAspHisAla  100
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Db   385  ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCCCATATAACACAGACCACGCG  444

Qy   101  GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrPheAspAlaLeu  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445  CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCTCCACCTTCGATGCTCTC  504

Qy   121  SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal  140
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Db   505  TCTCCATCACCCGCCATCCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG  564

Qy   141  SerPheGlnSerSerThrAlaLysSerAlaThrThrTyrSerThrGluLeuLys  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565  TCCTTCCAGAGCTCCACCGCCAAGTCGGCCACCACGTATTCCACTGAACTGAAG  624

Qy   161  LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625  AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy   181  ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685  CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG  744

Qy   201  ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745  GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC  804

Qy   221  ProProSerHisIleArgValGluAsnSerHisAlaGlnTyrValGluAspProCys  240
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Db   805  CCTCCTAGTCATTTGATTCGTGAGAATAGCCATGCCCAGTATGTAGAAGATCCC  864

Qy   241  IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
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Db   865  ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  924

Qy   261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
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Db   925  ACGACAGTCTTGTACAATTTCATGTGCAACAGTTGTTGTGGAGGAATGAACCGCCGT  984

Qy   281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
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Db   985  CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC  1044

Qy   301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle  320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045  TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGACAGGAAGGCGGATGAAGATAGCATC  1104

Qy   321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrArgProPheArg  340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105  AGAAAGCAACAGGTTTCGGACAGTACAAAGAACGGTGATGGTACGAGGCCCTTTCGT  1164

Qy   341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165  CAGAACACACATGGTATCCAGATGACATCCATCAAGAAAAGAAGATCCCCAGATGATGAA  1224

Qy   361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225  CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG  1284

Qy   381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285  TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACCATTGAAACGTACAGGCAACAGCAA  1344

Qy   401  GlnGlnGlnHisGlnHisLeuLeuGlnLysSerAlaCysProPheArgHisSerLys  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345  CAGCAGCAGCACCAGCACTTACTTCAGAAAATCTCCTTTCAGCCTGCTTCAGGAATGAG  1404

Qy   421  LeuValGluProArgArgArgProLysGlnSerAspValPhePheArgHisSerLys  440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1405  CTTGTGGAGCCCCGGAGAAGAAACTCCAAAACAATCTGACGTCTTCTTTAGACATTCCAAG  1464

Qy   441  ProProAsnArgSerValTyrPro  448
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;  CURRENT APPLICATION NUMBER: US/09/606,421B
;  CURRENT FILING DATE: 2000-06-28
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE: FastSEQ for Windows Version 3.0
;  SEQ ID NO 333
;  LENGTH: 2816
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-606-421B-333

Alignment Scores:
Pred. No.:
Score:                    1.13e-250           Length:        2816
Percent Similarity:       100.00%             Matches:        448
Best Local Similarity:    100.00%             Conservative:     0
Query Match:              100.00%             Mismatches:       0
DB:                                           Indels:           0
                                              Gaps:             0

US-09-670-568C-1 (1-448) x US-09-606-421B-333  (1-2816)

Qy    1  MetSerGlnSerThrThrArgGlnThrAsnLeuSerProLeuSerProGluValPheGlnHisIleTrp  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  145  ATGTCCCAGAGCACCACACAGACCAATGAATTCTCAGTCCCAGAGGTTTCCAGCATATCTGG  204

Qy   21  AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheLeuValAspHisGlu  40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  205  GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  264

Qy   41  ProSerGluAspGlyAlaThrAsnLysIleIleSerMetAspArgCysIleLeuArgMetGln  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  265  CCATCAGAGGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGATGCAG  324

Qy   61  AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuLeuAsnLeuLeuAsnSer  80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACAAACCTGGGGCTTCTGAACAGC  384

Qy   81  MetAspGlnGlnIleGluAsnGlySerSerSerProTyrAsnThrAspHisAla  100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  385  ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCCCATACAACACAGACCACGCG  444

Qy  101  GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAlaAspAlaAlaLeu  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  445  CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCAGCACCTTCGCTGCTCTC  504

Qy  121  SerProSerProAlaIleProSerAsnThrAspCysSerPheArgAspGluProPheArgAspVal  140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  505  TCTCCATCACCCGCCATCCCTTCCAACACCGACTGCTCCTTCAGAGATGAGCCGTTCCGAGATGTG  564

Qy  141  SerPheGlnGlnSerSerThrAlaAlaSerAlaThrTrpTyrSerThrGluLeuLeuLys  160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565  TCCTTCCAGCAGTCGAGCACCGCAGCGTCGGCCACGTATTCCACTGAACTGAAG  624

Qy  161  LysLeuTyrCysGlnIleAlaLysAlaThrProIleGlnIleLeuLysAlaLysThrProPro  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625  AAACTTCTACTGCCAAATTGCAAAGGCCAATCCGATCAGATTCAAGGTGATGACCCCACCT  684

Qy  181  ProGlnGlyAlaValAlaIleArgAlaMetProValTyrLysAlaGluHisValThrGlu  200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  685  CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTCACAAAAAGCTGAGCACGTCACGGAG  744

Qy  201  ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleIleAla  220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  745  GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC  804

Qy  221  ProProSerHisLeuIleArgValGluGluGlyAlaGluGlnSerHisAlaGlnTyrValGluAspPro  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  805  CCTCCTAGTCATTTGATTCGAGTAGAGGAGGGAAGCAGCCATGTGCCCAGTATGTAGAAGATCCC  864

Qy  241  IleThrGlyArgGlnSerValLeuValProGlnProGlnValGlyThrGluGlyPhe  260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  865  ATCACAGGAAGACAGAGTGTGCTGGTACCTCAGCCTCAGGTTGGCACTGAACTTGAAATTC  924

Qy  261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  925  ACGACAGTCCTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT  984
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Qy  281  ProIleLeuIleIleValThrArgLeuGluThrArgAspAspGlyGlnValLeuGlyArgArgCys  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  985  CCAATTTTAATCATTGTAACTCGTCTGGAAACCAGAGATGATGGCCAAGTCCTGGGCCGACGCTGC  1044

Qy  301  PheGluAlaAlaArgIleCysAlaCysProGlyArgAspArgLysThrGluGluAspSerIle  320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1045  TTTGAGGCCGCGATCTGTGCTGCCCAGGAGAAGACAGGAAGAGATAGAAGATAGCATC  1104

Qy  321  ArgLysGlnGlnValSerSerThrLysSerAsnGlyAspGlyThrArgProPheArg  340
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1105  AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACAACGGTGATGGTACGAGGCCCGTTTCGT  1164

Qy  341  GlnAsnThrHisGlyIleIleGlnMetThrSerIleLysSerLysArgArgSerProAspGlu  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1165  CAGAACACACACATGTATCCAGATGACATCCATCAAGAGAAAGAATCGAAGAAGATGATGAA  1224

Qy  361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLysIleGlu  380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1225  CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTTTTGAAGAAGATCGAAGAG  1284

Qy  381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1285  TCCCTGGAACTGATGCAGTACCTTCCTCAGCACACGATAGAAACGTATAGGCAACAGCAA  1344

Qy  401  GlnGlnGlnHisGlnHisLysHisLeuLeuGlnLysLysHisHisGlnLeuLeuSerLys  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1345  CAGCAGCAGCACCAGCACTTACTTCAGAAACATCTCCTTTCAGCCTGCTTTCAGGAATGAG  1404

Qy  421  LeuValGluProArgArgArgGluThrProLysLysProPhePheProArgHisSerArgLys  440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1405  CTTGTGGAGCCCCGGAGAAGAGAAACTCCAAAACAATTCCACGTGACGTCTCTTTAGACATTCCAAG  1464

Qy  441  ProProAsnArgSerValTyrPro  448
            ||||||||||||||||||||||||
Db 1465  CCCCCAAACCGATCAGTGTACCCA  1488
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RESULT 4
US-09-606-421B-333
; Sequence 333, Application US/09606421B
; Patent No. 6513315
; GENERAL INFORMATION:
; APPLICANT:  Wang, Tongtong
; APPLICANT:  Fan, Liqun
; APPLICANT:  Kalos, Michael D.
; APPLICANT:  Bangur, Chaitanya S.
; APPLICANT:  Hosken, Nancy
; APPLICANT:  Fanger, Gary R.
; APPLICANT:  Li, Samuel X.
; APPLICANT:  Wang, Aijun
; APPLICANT:  Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
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Query Match:    100.00%        Indels:   0
DB:             4              Gaps:     0

US-09-670-568C-1 (1-448) x US-09-630-940B-333 (1-2816)

Qy     1  MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp        20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145  ATGTCCCAGAGCACAGACAGAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG       204

Qy    21  AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu        40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   205  GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA       264

Qy    41  ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleSerArgMetGln    60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   265  CCATCAGAAGATGGTGCACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG       324

Qy    61  AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer       80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC      384

Qy    81  MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProSerTyrAsnThrAspHisAla   100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   385  ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCG      444

Qy   101  GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrProheAlaAlaLeu        120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   445  CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCACCCCTTCGATGCTCTC       504

Qy   121  SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal       140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   505  TCTCCATCACCCGCCATCCCTTCCAACACCGACTACCCCGGCCCACAGAGTTTCGACGTG      564

Qy   141  SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpProTyrSerThrGluLeuLys       160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   565  TCCTTCCAGCAGTCGAGCACCGCCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG      624

Qy   161  LysLeuTyrCysGlnIleAlaIleArgCysProIleGlnIleLysIleValMetThrProPro   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   625  AAACTCTACTGCCAAATTGCAAGAAGCATGCCCCATCCAGATCAAGGTGATGACCCCACCT    684

Qy   181  ProGlyGlyAlaAlaValIleLeuArgGlnAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685  CCTCAGGGAGCTGTTATCCTGCGCCATGCCATGCCTGTCTACAAAAAGCTGAGCACGTCACGGAG  744

Qy   201  ValValTyrArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla       220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745  GTGGTGAAGCGTGCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC       804

Qy   221  ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro       240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   805  CCTCCTAGTCATTTGATTCGAGTAGAGGGAAACAGCCATGCCCAGTATGTAGAAGATCCC      864

Qy   241  IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe       260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   865  ATCACAGGAAGACAGAGTGTCTTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC      924

Qy   261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg       280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925  ACGACAGTCTTGTACAATTTCATGTGCAACTCGTCTTGTGTTGGAGGGATGAACCGCCGT      984

Qy   281  ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys       300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985  CCAATTTTAATCATTGTTACTCTGGAAACACGAGATGGGCCAGTCCTGGGCCGACGCGCTGC    1044

Qy   301  PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle       320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045  TTTGAGGCCCGGATCTGTGCTTGTCCCAGGAGAGACAGGAAGGCGGATGAAGATAGCATC     1104

Qy   321  ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg       340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1105  AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT     1164

Qy   341  GlnAsnThrHisGlyIleGlnMetThrSerIleLysMetThrSerIleLysLysArgArgSerProAspAspGlu 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1165  CAGAACACACATGGTATCCAGATGACATCCATCAAGAAAACAGAAGATCCCCAGATGATGAA   1224

Qy   361  LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleSerGlu       380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1225  CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG     1284

Qy   381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln       400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1285  TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA    1344

Qy   401  GlnGlnGlnHisGlnHisGlnLysLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1345  CAGCAGCAACACCAGCACTTACTTCAGAAACATCTCCTTCAGCCTGCTTCCAGGAATGAG    1404

Qy   421  LeuValGluProArgArgGluThrProLysGlnSerAspAspValPhePheHisSerLys       440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1405  CTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGTCTTCTTTCATTCCAAG       1464

Qy   441  ProProAsnArgSerValTyrPro      448
          |||||||||||||||||||||||
Db  1465  CCCCCAAACCGATCAGTGTACCCA     1488
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RESULT 5

US-09-630-940B-333

; Sequence 333, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-333

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Alignment Scores:
Pred. No.:              1.13e-250      Length:        2816
Score:                  2383.00        Matches:       448
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
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Qy 121 CCATCAGAAGATGGTGCGACAAACAAGATTGAGACTGTATCCGCATGCAG 180
Db   61 AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuGlyLeuLeuAsnSer   80
Db 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGACTTACACCAACCTGGGCTTCCTGAACAGC 240

Qy   81 MetAspGlnGlnIleGlnAsnGlySerSerThrSerProTyrAsnThrAspHisAla 100
Qy 241 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCGTCCCTATAACACAGACCACGCG 300

Db 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrPheAlaAspAlaLeu 120
Db 301 CAGAACAGCGTCACGGCGCCTTCGCCCTACGCACAGCCCAGCTCCACCTTCGATGCTCTC 360

Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Qy 361 TCTCCATCACCCGCCATCCCTTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG 420

Db 141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 421 TCCTTCCAGAGTCGAGCACCGCCAAGTCGGCACCTGGACGTATTCCACTGAACTGAAG 480

Qy 161 LysLeuTyrCysGlnIleAlaAlaLysThrCysProIleGlnIleLeuLysValMetProPro 180
Qy 481 AAACTTCTACTGCCAAATTCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT 540

Db 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaAlaHisValThrGlu 200
Db 541 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG 600

Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Qy 601 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC 660

Db 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 661 CCTCCCAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC 720

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnLeuValGlyThrGluPhe 260
Qy 721 ATCACAGGAAGACAGAGTGTGGTACCTTATGAGCCACCCCAGGTTGCACTGAATTC 780

Db 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 781 ACGACAGTCTTGTACAATTCATGTGTAACAGCAGTTGTTGGTGGGGATGAACCGCCGT 840

Qy 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyValGlnLeuGlyArgArgCys 300
Qy 841 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGCCAAGTCCTGGGCCGACGCTGC 900

Db 301 PheGluAlaArgIleCysSerAlaCysProGlyArgAspArgLysAlaAspSerIle 320
Db 901 TTTGAGGCCCGGATCTGTTCGTGCTTGCCCAGGAAGAGACCAGGAGGCGGATGAAGATAGCATC 960

Qy 321 ArgLysGlnGlnValSerAspAspSerThrLysAsnGlyAspGlyThrLysProPheArg 340
Qy 961 AGAAAGCAGCAAGTTTCGACAGTACAAAGAACGGTGATGGTACAAGCCCCGTTTCGT 1020

Db 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLeuLysArgGluThrTyrGluMetLeuLysLysGlu 360
Db 1021 CAGAACACACATGGTATCCAGATGACAATCCATCAAGAAACGAGAAACCTGGGATGATGAA 1080

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLysLysGlu 380
Qy 1081 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1140

Db 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1141 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACCAATTGAAACGTACACAGCAACAGCAA 1200

Qy 401 GlnGlnHisGlnHisHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Qy 1201 CAGCAGCAGCAGCCAGCACTTACTTCAGAA----------- 1230

Db 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLeuLysArgArgSerProAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACAATCCATCATCAAGAAACGAGAAACCCAGATGATGAA 1224

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLysLysGlu 380
Qy 1225 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Db 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
Db 1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACCAATTGAAACGTACACAGGCAACAGCAA 1344

Qy 401 GlnGlnHisGlnHisHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Qy 1345 CAGCAGCAGCAGCCAGCACTTACTTCAGAAAACATCCTCTTCAGCCTGCTGCTTCAGGAATGAG 1404

Db 421 LeuValGluProArgArgGluThrProLysSerAspValPhePheArgPheLysHisSerLys 440
Db 1405 CTTTGTGGAGCCCCGGAGAGAAACTCCAAAACAATCCGAGTCTTCTTCTTTAGACATTCCAAG 1464

Qy 441 ProProAsnArgSerValTyrPro 448
Qy 1465 CCCCCAAACCGATCAGTGTACCCA 1488

RESULT 6
US-09-643-597-337

; Sequence 337, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Fan, Liqun
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Hosken, Nancy
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Li, Samuel X.
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: McNeill, Patricia D.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.455C11
;   CURRENT APPLICATION NUMBER: US/09/643,597
;   CURRENT FILING DATE: 2000-08-21
;   NUMBER OF SEQ ID NOS: 369
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-337

Alignment Scores:
Pred. No.:   2.21e-229   Length: 1551
Score: 2185.00   Matches: 416
Percent Similarity: 94.80%   Conservative: 3
Best Local Similarity: 94.12%   Mismatches: 7
Query Match: 91.69%   Indels: 16
DB: 3   Gaps: 1

US-09-670-568C-1 (1-448) x US-09-643-597-337 (1-1551)

Qy   1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db   1 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 60

Qy 21 AspPheLeuGlnGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 61 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA 120

Qy 41 ProSerGluAspAspGlyAlaThrAsnLysIleGluIleGluSerMetAspCysSerArgMetGln 60

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Qy  421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
                                        :::  ::   : :::
Db 1231 ------------------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC 1272

Qy  441 ProPro 442
            ||
Db 1273 CCACCT 1278
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RESULT 7
US-09-542-615A-337
; Sequence 337, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-337

Alignment Scores:
Pred. No.:   2.21e-229   Length: 1551
Score: 2185.00   Matches: 416
Percent Similarity: 94.80%   Conservative: 3
Best Local Similarity: 94.12%   Mismatches: 7
Query Match: 91.69%   Indels: 16
DB: Gaps: 4

US-09-670-568C-1 (1-448) x US-09-542-615A-337 (1-1551)

Qy   1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 60

Qy   21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspAspLeuAsnPheValAspGlu 40
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATTTTCTGGAACAGCCTATATGTCAGTTCAGTTGAACTTTGTGGATGAA 120

Qy   41 ProSerGluAspGlyAlaThrAsnLysSerIleGluIleSerMetAspCysIleArgMetGln 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG 180

Qy   61 AspSerAspAspLeuSerAspAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GACTCGGACGACCTGAGTGACGACCCCATGTGGCCACAGTACACGAACCTGGGCCTCCTGAACAGC 240

Qy   81 MetAspAspGlnIleLeuAspAsnGlySerSerThrSerProSerTyrAsnThrAspHisAla 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 ATGGACGACCAGATTCAGAACGGCTCCTCCGTCCACCAGTCCCTATAACACAGACCACGCG 300

Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 CAGAACAGCGTCACGGCGCCGTCCCCGTACGCCCAGCCTAGCAGCACCTTCGATGCTCTC 360

Qy 121 SerProSerProAlaIleGluProSerAspAsnThrAspProTyrProHisSerProAspVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 TCTCCATCACCCGCCATCCCCTCCGACAACACCGACCCTTACCCAGCCCGCACAGTTTCGACGTG 420

Qy 141 SerPheGlnGlnSerSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TCCTTCCAGAGTCGAGCAGCACCGCCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG 480

Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 AAACTCTACTGCCAAATTGCAAAGACATGCCCATCCAGATCAAGGTGATGACCCCACCT 540

Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 CCTCAGGGAGCTGTTATCCGGGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG 600

Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyIleIleAla 220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC 660

Qy 221 ProProSerHisLeuLeuArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACATGCCCAGTATGTAGAAGATCCC 720

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 780

Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT 840

Qy 281 ProIleLeuIleIleLeuValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC 900

Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysThrGluGluGlyAspSerIle 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 901 TTTGAGGCCCGGATCTGTGCTTGCCCCGGAAGAGACAGGAAGACAGAAGAGGGCGATGAAGATAGCATC 960

Qy 321 ArgLysGlnValSerAspSerThrLysLysAsnGlyAspGlyThrLysArgProPheArg 340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 961 AGAAAGCAGGTAAGTTTCGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT 1020

Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgSerArgProAspAspGlu 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1080

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLeuLysGlu 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CTGTTATATCTTCCACCGTGAGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1140

Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1200

Qy 401 GlnGlnGlnHisGlnHisGlnHisGluGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
          |||||||||||||||||||||||||||||
Db 1201 CAGCAGCAGCACCAGCACTTACTTCAGAAA----------------------- 1230

Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
                                        ::: ::   : :::
Db 1231 ------------------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC 1272

Qy 441 ProPro 442
            ||
Db 1273 CCACCT 1278
```

RESULT 8
US-09-606-421B-337
; Sequence 337, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.

```
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-337

Alignment Scores:
Pred. No.:              2.1e-229        Length:        1551
Score:                  2185.00         Matches:       416
Percent Similarity:     94.80%          Conservative:  3
Best Local Similarity:  94.12%          Mismatches:    7
Query Match:            91.69%          Indels:        16
DB:                     4               Gaps:          1

US-09-670-568C-1 (1-448) x US-09-606-421B-337 (1-1551)

Qy    1 MetSerGlnThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisHisTrp   20
Db    1 ATGTCCCAGACGCACCAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  60

Qy   21 AspPheLeuGluCysSerValGlnProIleAspLeuAsnPheValAspGlu           40
Db   61 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA 120

Qy   41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln  60
Db  121 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG 180

Qy   61 AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db  181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGACAACCTGGGGCTCCTGAACAGC      240

Qy   81 MetAspGlnGlnIleGlnAsnGlySerSerSerProLeuSerProTyrAsnThrAspHisHisAla 100
Db  241 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCTCCACCAGTCCTATAACACAGACCACGCG 300

Qy  101 GlnAsnSerValThrAlaProSerProTyrArgAlaGlnInProSerSerThrPheAspAlaLeu 120
Db  301 CAGAACAGCGTCACGGCGCCCTCGCCCTACCGCGCACAGCCCAGCTCCACCTTCGATGCTCTC 360

Qy  121 SerProSerProAlaIleProAlaSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db  361 TCTCCATCACCCGCCATCCCCGCCAGCAACACCGACTACCCAGGCCCCCACAGTTTCGACGTG 420

Qy  141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys    160
Db  421 TCCTTCCAGAGCAGTACCGCGAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG    480

Qy  161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db  481 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT 540

Qy  181 ProGlnGlyAlaValIleLeuArgGlaMetProValThrTyrLysLysAlaGluHisValThrGlu 200
Db  541 CCTCAGGGAGCTGTTATCCGGCCATGCCAGTGACGCACGTCACGGAG              600

Qy  201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleIleAla 220
Db  601 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC 660

Qy  221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db  661 CCTCCCAGTCATTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTGAAGGATCCC 720

Qy  241 IleThrArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe   260
Db  721 ATCACAGGAAGCAGAGAGTGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 780

Qy  261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db  781 ACGACAGTCTTGTACAATTCATGTGTAACAGCAGTGTGTTGGAGGATGAACCGCGCGT  840

Qy  281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db  841 CCAATTTAATCATTGTTACTCTGGAAACACGAGATGGGCAAGTCCTGGGCCGACGCTGC  900

Qy  301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaGluAspSerIle   320
Db  901 TTTGAGGCCCGGATCTGCGCTTGCCCAGGAAGAGACAGGAAGGCGGATGAAGATAGCATC 960

Qy  321 ArgLysGlnGlnValSerAspSerThrLysArgAspGlyThrLysArgProPheArg   340
Db  961 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAAGAACGGTACGGAGCCGCCCGTTTCGT 1020

Qy  341 GlnAsnThrHisGlyIleGlnMetThrSerIleLeuLysArgArgSerProAspAspGlu 360
Db 1021 CAGAACACACATGGTATCCAGATGACCATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1080

Qy  361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLeuLysGlu 380
Db 1081 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1140

Qy  381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1141 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1200

Qy  401 GlnGlnGlnHisGlnHisGlnLeuGlnLysSerLeuLeuGlnSerAlaCysPheArgAsnGlu 420
Db 1201 CAGCAGCAGCACCAGCACTTACTTCAGAAA                              1230

Qy  421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1231 ------------------------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC 1272

Qy  441 ProPro                                                      442
Db 1273 CCACCT                                                     1278
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```
RESULT 9
US-09-630-940B-337
; Sequence 337, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-337
```

Alignment Scores:
Pred. No.:   2.21e-229
Score: 2185.00
Percent Similarity: 94.80%
Best Local Similarity: 94.12%
Query Match: 91.69%
DB: 4

	Length:	1551	
	Matches:	416	
	Conservative:	3	
	Mismatches:	7	
	Indels:	16	
	Gaps:	1	

US-09-670-568C-1 (1-448) x US-09-630-940B-337 (1-1551)

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Qy     1 MetSerGlnThrArgGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp  20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGTCCCAGACGAGCACAGACAAATGAATTCCTGAGTCCAGAGGTTTTCCAGCATATCTGG  60

Qy    21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu  40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGACTTTGTGGATGAA  120

Qy    41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG  180

Qy    61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer  80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GACTCCGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC  240

Qy    81 MetAspGlnGlnIleGlnAsnGlySerSerSerSerProTyrAsnThrAspHisAla  100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCTCCACCAGTCCTATAACAGACCACGCG  300

Qy   101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrPheAspAlaLeu  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAGAACAGCGTCACGGCCCCTACGCCCTACGCCCAGCCCAGTCCCACCTTCGATGCTCTC  360

Qy   121 SerProSerProAlaIleProLeuProSerAsnThrAspTyrProGlyProHisSerPheAspVal  140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TCTCCATCACCCGCCATCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG  420

Qy   141 SerPheGlnSerSerThrAlaLysSerAlaThrArgThrTyrSerThrGluLeuLys  160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCCTTCCAGAGCAGTACAGCTAAGAGTGCCACCCGGACGTATTCCACTGAACTGAAG  480

Qy   161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAACTCTACTGCCAAATTGCCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  540

Qy   181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysLysAlaGluHisValThrGlu  200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAGTCAGACATGCACGGAG  600

Qy   201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC  660

Qy   221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspProPro  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CCTCCCAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTGGAAGATCCC  720

Qy   241 IleThrThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  780

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGGCGT  840

Qy   281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CCAATTTAAATCATTGTTACTCTGGAAACCAGAGATGGCAGTCCTGGGCACCGCTGC  900

Qy   301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgAlaAspGluAspSerIle  320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145 ATGTCCCAGACGAGCACAGACAAATGAATTCCTGAGTCCAGAGGTTTTCCAGCATATCTGG  204
```

```
Db   901 TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGACAGGAGGCGGATGAAGATAGCATC  960
Qy   321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT  1020

Qy   341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgSerProAspAspGlu  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CAGAACACACATGTATCCAGATGACATCCATCAAGAACGAAGATCCCCAGATGATGAA  1080

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CTGTTATACTTACCAGTGCGAGGGGCCGTGAGACTTATGAAATGTGTTGAAGATCAAGAG  1140

Qy   381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TCCCTGGAACTCATGCAGTACTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA  1200

Qy   401 GlnGlnHisGlnHisHisGlnLysHisLeuLeuArgAlaCysPheArgAsnGlu  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 CAGCAGCAGCACCAGCACTTACTTCAGAAA  1230

Qy   421 LeuValGluProArgArgGluThrProGlnSerAspValPhePheArgPheHisSerLys  440
           ||                                   |::  |||||||||||
Db  1231 -----------------------------CAGACCTCAATACAGTCTCCATCTTCATATGTAACAGCTCC  1272

Qy   441 ProPro  442
           ||||||
Db  1273 CCACCT  1278
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RESULT 10
US-09-643-597-332
; Sequence 332, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;   APPLICANT: Wang, Tongtong
;   APPLICANT: Fan, Liqun
;   APPLICANT: Kalos, Michael D.
;   APPLICANT: Bangur, Chaitanya S.
;   APPLICANT: Hosken, Nancy
;   APPLICANT: Fanger, Gary R.
;   APPLICANT: Li, Samuel X.
;   APPLICANT: Wang, Aijun
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Henderson, Robert A.
;   APPLICANT: McNeill, Patricia D.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;   FILE REFERENCE: 210121.455C11
;   CURRENT APPLICATION NUMBER: US/09/643,597
;   CURRENT FILING DATE: 2000-08-21
;   NUMBER OF SEQ ID NOS: 369
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 332
;   LENGTH: 2270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-643-597-332

Alignment Scores:
Pred. No.:   4.16e-229
Score: 2185.00
Percent Similarity: 94.80%
Best Local Similarity: 94.12%
Query Match: 91.69%
DB:

	Length:	2270	
	Matches:	416	
	Conservative:	3	
	Mismatches:	7	
	Indels:	16	
	Gaps:	1	

US-09-643-597-332 (1-448) x US-09-643-597-332 (1-2270)

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Qy     1 MetSerGlnThrArgGlnThrAsnGluPheLeuSerProGluLeuValPheGlnHisIleTrp  20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   145 ATGTCCCAGACGAGCACAGACAAATGAATTCCTGAGTCCAGAGGTTTTCCAGCATATCTGG  204
```

```
Qy     21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu    40
Db    205 GATTTTCTGAACAGCCTATATGTTCAGTTCAGCCTGTTCAGCTGTGCGATGAA           264

Qy     41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln    60
Db    265 CCATCAGAGATGGTGGCACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG    324

Qy     61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyIleLeuAsnSer    80
Db    325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACAAACTTGGGCTCCTGAACAGC    384

Qy     81 MetAspGlnGlnIleGlnAsnGlySerSerSerProTyrAsnThrAspHisAla       100
Db    385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCCACCAGTCCCTATAACAGACCACGCG   444

Qy    101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerProTyrAlaGlnAlaLeu   120
Db    445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCTCCACCTTCGATGCTCTC     504

Qy    121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheVal     140
Db    505 TCTCCATCACCCGCCATCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG   564

Qy    141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys     160
Db    565 TCCTTCCAGTCCAGTACCGCCAAGTCGGCCACCTGGACGTATTCCACTGAACTGAAG    624

Qy    161 LysLeuTyrCysGlnIleAlaLysThrCysProIleLeuLysValMetThrProPro    180
Db    625 AAACTCTACTGCCAAATTGCAAAGACCATGCCCATCCAGATCAAGGTGATGACCCCACCT   684

Qy    181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu   200
Db    685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAGGCTGAGCACGTCACGGAG   744

Qy    201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla   220
Db    745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC   804

Qy    221 ProProSerHisLeuIleArgValGluValGluGlyAsnSerHisAlaGlnTyrValGluAspPro   240
Db    805 CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC   864

Qy    241 IleThrGlyArgGlnSerValLeuValProTyrGlnProProGlnValGlyThrGluPhe   260
Db    865 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC   924

Qy    261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg     280
Db    925 ACGACAGTTCTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT   984

Qy    281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys   300
Db    985 CCAATTTTAATCATTGTAACTCTCGAAACCAGAGATGGCCAGGTCCTGGGCCGGCGCTGC   1044

Qy    301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgThrGluGluGluAspSerIle   320
Db   1045 TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGAGACAGGAGGACAGAAGAAGATAGCATC   1104

Qy    321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg   340
Db   1105 AGAAAGCAGCAAGTTTCGGACAGTACAAGAACGGTGATGGTACGAAGCGCCCCGTTTCGT   1164

Qy    341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu   360
Db   1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAGCGAAGATCCCCAGATGATGAA   1224

Qy    361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu   380
Db   1225 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTTTTGAAGATCAAAGAG   1284

Qy    381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln   400
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```
Db   1285 TCCTTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGCAGCAGCAA  1344
Qy    401 GlnGlnGlnHisGlnHisLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu   420
Db   1345 CAGCAGCAGCACCAGCACTTACTTCAGAAA                              1374
Qy    421 LeuValGluProArgArgGluThrProGlnSerAspValPhePheArgHisSerLys   440
Db   1375 --------------CAGACCTCAATACAGTCTTCATCTTCATATGGTAACAGTCC     1416
Qy    441 ProPro 442
Db   1417 CCACCT 1422
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RESULT 11
US-09-542-615A-332
; Sequence 332, Application US/09542615A
; Patent No. 651825&
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-332

```
Alignment Scores:
  Pred. No.:                    4.16e-229        Length:           2270
  Score:                        2185.00          Matches:           416
  Percent Similarity:           94.80%           Conservative:        3
  Best Local Similarity:        94.12%           Mismatches:          7
  Query Match:                  91.69%           Indels:             16
  DB:                           4                Gaps:                1
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US-09-670-568C-1 (1-448) x US-09-542-615A-332 (1-2270)

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Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp    20
Db    145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG   204

Qy     21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu    40
Db    205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCTATTGACTTTGTGGATGAA        264

Qy     41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln    60
Db    265 CCATCAGAGATGGTGGCACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG    324

Qy     61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer    80
Db    325 GACTCGGACCTGAGTGACCCCATGTGGCCCCAGTACACCAACTTGGGCCTCCTGAACAGC   384

Qy     81 MetAspGlnGlnIleGluAsnGlyGlySerSerProTyrAsnThrAspHisAla       100
Db    385 ATGGACCAGCAGATTCAGAACGGCGGCTCCTCGTCCCATAAACAGACCACCACGCG     444

Qy    101 GlnAsnSerValThrAlaProSerProTyrAlaProProTyrProSerThrPheAspAlaLeu   120
Db    445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCCCCAGCTCCACCTTCGATGCTCTC  504
```

```
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C9
;  CURRENT APPLICATION NUMBER: US/09/606,421B
;  CURRENT FILING DATE:  2000-06-28
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE:  FastSEQ for Windows Version 3.0
;  SEQ ID NO 332
;    LENGTH: 2270
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-606-421B-332

Alignment Scores:
Pred. No.:                        4.16e-229  ;  Length:              2270
Score:                            2185.00    ;  Matches:             416
Percent Similarity:               94.80%     ;  Conservative:        3
Best Local Similarity:            94.12%     ;  Mismatches:          7
Query Match:                      91.69%     ;  Indels:              16
DB:                               4          ;  Gaps:                1

US-09-670-568C-1 (1-448) x US-09-606-421B-332  (1-2270)
```

```
Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 ATGTCCCAGAGCACCAGACAAACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCGG  204

Qy     21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu   40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA  264

Qy     41 ProSerGluAspGlyAlaThrArgLysIleGluIleLeuSerMetAspCysIleArgMetGln   60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 CCATCAGAAGATGGTGCGACAAGATTGAGATTAGCATGGACTGTATCCGGATGCAG  324

Qy     61 AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuGlyLeuLeuAsnSer   80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGACTTACACCAACCTGGGGCTCCTGAACAGC  384

Qy     81 MetAspGlnGlnIleGlnAsnGlyLysSerSerThrSerProTyrAsnThrAspHisAla  100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 ATGGACCAGCAGATTCAGAACGGCGTCCTCGTCCCTATAACACAGACCACCACGCG  444

Qy    101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrProAspAlaLeu  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CAGAACAGCGTCACGGGCCGCCTCCCCTACGCACAGCCCAGCACCCCAGATGCTCTC  504

Qy    121 SerProSerProAlaIleProSerAsnThrAspTyrProHisSerPheAspVal  140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 TCTCCATCACCCGGCCATCCCTCCAACACCGACTACCCCACCAGTTTCGACGTG  564

Qy    141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys  160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 TCCTTCCAGTCGAGCACCGCCAGTGCGACGTATTCCACTGAACTGAAG  624

Qy    161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy    181 ProGlnIleAlaValIleArgArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 CCTCAGGGAGCTGTTATCCGGCGCCATGCCGTGTCTCACAAAAAGTGAGCAGTCACGGAG  744

Qy    201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
```

```
Qy    121 SerProSerProAlaIleProSerAsnThrAspTyrProHisSerPheAspVal  140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 TCTCCATCACCCGGCCATCCCTCCAACACCGACTACCCCACCAGTTTCGACGTG  564

Qy    141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys  160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 TCCTTCCAGTCGAGCACCGCCAGTGCGACGTATTCCACTGAACTGAAG  624

Qy    161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy    181 ProGlnIleAlaValIleArgArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 CCTCAGGGAGCTGTTATCCGGCGCCATGCCGTGTCTCACAAAAAGTGAGCAGTCACGGAG  744

Qy    201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 CCTTCCAGTCGTCATTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCC  864

Qy    221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrTyrValGluAspPro  240

Qy    241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865 ATCACAGGAAGACAGAGTGTCTGGTACCTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  924

Qy    261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 ACGACAGTCCTGTACAATTTCATGTGTAACACAGTTGTGTTGGAGGGATGAACCGCCGT  984

Qy    281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGCGTGC  1044

Qy    301 PheGluLeuAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluSerIle  320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 TTTGAGGCCCGGATCTGTGCTTGCCCAGGAAGACAGGAGGAGATGAAGATAGCATC  1104

Qy    321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg  340
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT  1164

Qy    341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 CAGAACACACACGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA  1224

Qy    361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 CTGTTATACTTACCAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG  1284

Qy    381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA  1344

Qy    401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1345 CAGCAGCAGCACCAGCACTTACTTCAGAAA--------------------------  1374

Qy    421 SerPheGlnSerGlnSerAspValPhePheArgHisSerPheLys  440
            ||||||           ::   :::||||
Db   1375 ---------------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC  1416

Qy    441 ProPro  442
            ||||||
Db   1417 CCACCT  1422
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```
Qy    121 SerProSerProAlaIleProSerAsnThrAspTyrProHisSerPheAspVal  140
Db    505 TCTCCATCACCCGGCCATCCCTCCAACACCGACTACCCCACCAGTTTCGACGTG  564

Qy    141 SerPheGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys  160
Db    565 TCCTTCCAGTCGAGCACCGCCAGTGCGACGTATTCCACTGAACTGAAG  624

Qy    161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
Db    625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy    181 ProGlnIleAlaValIleArgArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
Db    685 CCTCAGGGAGCTGTTATCCGGCGCCATGCCGTGTCTCACAAAAAGTGAGCAGTCACGGAG  744

Qy    201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
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RESULT 12
US-09-606-421B-332
; Sequence 332, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-332

Alignment Scores:
Pred. No.:   4.16e-229   Length: 2270
Score: 2185.00   Matches: 416
Percent Similarity: 94.80%   Conservative: 3
Best Local Similarity: 94.12%   Mismatches: 7
Query Match: 91.69%   Indels: 16
DB: Gaps: 1

US-09-670-568C-1 (1-448) x US-09-630-940B-332 (1-2270)

```
Qy    1  MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
Db  145  ATGTCCCAGAGCACCAGACAATGAATTCCTCAGTCAGTTTTTCCAGCATATCTGG       204

Qy   21  AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu   40
Db  205  GATTTCTTGGAACAGCCTATATGTTCAGTTCAGTTTGGGAACTTGAACTTTGTGATGAA   264

Qy   41  ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln   60
Db  265  CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG   324

Qy   61  AspSerAspLeuSerAspProMetTrpProGlnThrTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db  325  GACTCGGACCTGAGTGACCCCATGTGGCCACAGACATACACAAACCTGGGGCTCCTGAACAGC 384

Qy   81  MetAspGlnIleAsnGlyAsnSerSerSerThrSerProTyrAsnThrArgHisAla    100
Db  385  ATGGACCAGATTCAGAAGGGCTCCTCGTCCCCATAAACACAGACCACCGCG          444

Qy  101  GlnAsnSerValThrAlaProProTyrArgAlaGlnProSerSerThrPheAspAlaLeu  120
Db  445  CAGAACAGCGTCACGGCGCCTCCCTACCGCGCCCAGCCTTCCACCTTCGATGCTCTC    504

Qy  121  SerProProProAlaIleProAspGluAsnThrAspPTyrProGlyHisSerPheAspVal  140
Db  505  TCTCCATCACCCGCCATCCCTGACGAGAATACCGACTACCCAGGCCACAGTTTCGACGTG  564

Qy  141  SerPheGlnGlnSerSerThrAlaLysSerThrCysProIleGluAlaLysLysTrpTyrSerThrTyrSerThrGluLeuLys 160
Db  565  TCCTTCCAGCAGTCGAGCACCGCAAGTCGGCCACCTGACGATTCCACTGACTGAAG      624

Qy  161  LysLeuTyrCysGlnIleIleAlaLysSerThrCysProIleGluIleLeuLysValMetThrProPro 180
Db  625  AAACTCTACTGCCAAATTGCAAAGACAACATGCCCCATCCAGATCAAGGTGATGACCCCACCT 684

Qy  181  ProGlnGlyAlaValIleArgGluAlaMetAlaMetProValTyrLysLysAlaAlaGluHisValAlaThrGlu 200
Db  685  CCTCAGGGAGCTGTTATCCGGGCCATGGCCATGCCTGTTTATCACAAAAAGTCACGGAG   744

Qy  201  ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyIleIleAla  220
Db  745  GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGACAGATTGCC   804

Qy  221  ProProSerHisLeuIleArgValGluLeuValAsnSerHisAlaGlnTyrValGluAspPro 240
Db  805  CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACGCCATGCCCAGTAGTGTAACGAGATCCC 864

Qy  241  IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
Db  865  ATCACAGGAAGACAGAGTGTCTGGTACCTTGATGAGCCACCCCAGGTTGCACTGAATTC  924

Qy  261  ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg     280
Db  925  ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTGTGTTGGAGGATGAACCGCGT    984

Qy  281  ProIleLeuIleLeuValThrLeuGlnValThrArgAspGlyGlnValLeuGlyValArgArgCys 300
Db  985  CCAATTTTAATCATTGTTACTCTGCAAGTCACCAGAGATGGGCAAGTCCTGGGCGTGACGCGCTGC 1044

Qy  301  PheGluAlaArgIleCysAlaCysSerProGlyArgAspArgLysProGlyGlnAlaAspGluAspSerIle 320
Db 1045  TTTGAGGCCCGGATCTGTGCTTGCTCCCCAGGAAGAGACAGGAAGCCGGATGAAGATAGCATC 1104

Qy  321  ArgLysGlnGlnValSerAspArgSerThrLysAsnGlyAspGlyAspGlyThrLysArgProPheArg 340
Db 1105  AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGACGAACGCGCCGTTTCGT 1164

Qy  341  GlnAsnThrHisGlyIleGlnMetThrSerIleLeuTyrIleGlnMetLysIleLeuLysLysSerProAspAspGlu 360
Db 1165  CAGAACACACAGTATCCAGATGACATCCATCAAGAAACGAAGATCCCAGATGATGAA   1224

Qy  361  LeuLeuTyrLeuProValAlaArgGlyValArgGluThrTyrGluMetLeuLeuLysIleLeuLysGlu 380
Db 1225  CTGTTATACTTACCAGTGAGGGGCGTGAGACTTATGAAGATCAAAGAG           1284

Qy  381  SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285  TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy  401  GlnGlnGlnHisGlnHisLeuLeuLeuGlnLysHisHisLysSerPheAlaCysPheArgArgAsnGlu 420
Db 1345  CAGCAGCAGCACCAGCACTTACTTACAGAAA                            1374

Qy  421  LeuValGluProArgGluThrProLysProGlnSerAspValPheArgHisSerLys   440
Db 1375  ----------CAGACCCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC      1416

Qy  441  ProPro  442
Db 1417  CCACCT  1422
```

RESULT 13
US-09-630-940B-332
; Sequence 332, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630,940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367

US-09-643-597-335 (1-448) x US-09-643-597-335 (1-4849)

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Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp   20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG  204

Qy     21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu   40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGACTTTGTGGATGAA  264

Qy     41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG  324

Qy     61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer   80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 GACTCCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC  384

Qy     81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 ATGGACCAGCAGATTCAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCG  444

Qy    101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrProAspAlaProAsnAlaLeu  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGTACCCCACCTTCGATGCTCTC  504

Qy    121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal  140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505 TCTCCATCACCCGGCCATCCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG  564

Qy    141 SerPheGlnSerSerThrAlaLysSerAlaThrThrThrTyrSerAlaThrThrGluLeuLys  160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565 TCCTTCCAGAGTCGAGCACCCCAAGTCGGCACCTGACGTATTCCACTGAACTGAAG  624

Qy    161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625 AAACTTCTACTGCCAAATTGCAAAGACACATGCCCCATCCAGATCAAGGTGATGACCCCACCT  684

Qy    181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 CCTCAGGGAGCTGTTATCCGGCCAATGCCTGTCTACAAAAAAGTGAGCACGTCACGGAG  744

Qy    201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla  220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 GTGGTGAAGCGGTGCCCCAACATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC  804

Qy    221 ProProSerHisGluLeuArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    805 CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC  864

Qy    241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe  260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    865 ATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC  924

Qy    261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg  280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 ACGACAGTCTTGTACAATTTCATGTGTAACACAGTCAGTTGTGTGTTGGAGGGATGAACCGCCGT  984

Qy    281 ProLeuLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACCGTGC  1044

Qy    301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysArgLysAspGluSerIle  320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 TTTGAGGCCCGGATCTGCGCTTGCCCAGGAAGAGACAGAGGGCGATGAAGATAGCATC  1104

Qy    321 ArgLysGlnGlnValSerAspSerThrLysArgGlyThrLysAsnGlyThrLysArgProPheArg  340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGATGTGATGGTACGAAGCGCCCCGGTTTCGT  1164

Qy    341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db   1165 CAGAACACACATGGTATCCCAGATGACATCCATCAAGAAAACGAAGAAGATGATGAA  1224
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Qy    281 ProLeuLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACCGTGC 1044

Qy    301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysArgLysAspGluSerIle  320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1045 TTTGAGGCCCGGATCTGCGCTTGCCCAGGAAGAGACAGAGGGCGATGAAGATAGCATC   1104

Qy    321 ArgLysGlnGlnValSerAspSerThrLysArgGlyThrLysAsnGlyThrLysArgProPheArg  340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGATGTGATGGTACGAAGCGCCCCGGTTTCGT 1164

Qy    341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1165 CAGAACAGCAGCAGCCAGCCACCACTTACTTCAGAAC                         1224

Qy    361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu  380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1225 CTGTTATACTTACCAGTGAGGGGGCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy    381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln  400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy    401 GlnGlnGlnHisGlnHisLeuLeuGlnLysLysHisLeuLeuSerLeuGlnLysAsnGlu  420
          ||||||||||||||||||||||||||||||||||||||
Db   1345 CAGCAGCAGCAGCACCAGCACTTACTTCAGAAA-----                       1374

Qy    421 LeuValGluProArgArgGluThrProLysGlnSerAspValPheAspValPheAspHisSerLys  440
          :::||
Db   1375 --------------------------------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC 1416

Qy    441 ProPro  442
          ||||||
Db   1417 CCACCT  1422
```

RESULT 14
US-09-643-597-335

; Sequence 335, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-335

Alignment Scores:
Pred. No.:   1.46e-228   Length: 4849
Score: 2185.00   Matches: 416
Percent Similarity: 94.80%   Conservative: 3
Best Local Similarity: 94.12%   Mismatches: 7
US-09-643-597-335   91.69%   Indels: 16
Query Match: 3   Gaps: 1
DB:

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGlnMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATACTTACCAGTGAGGGCCCTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy   381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy   401 GlnGlnGlnHisGlnHisLeuLeuLeuGlnLysHisLeuLeuSerLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCACCAGCACTTACTTCAGAA------ 1374

Qy   421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1375 ----------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC 1416

Qy   441 ProPro 442
Db 1417 CCACCT 1422

RESULT 15
US-09-542-615A-335

; Sequence 335, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-335

Alignment Scores:
Pred. No.:
Score: 2185.00   Length: 4849
Percent Similarity: 94.80%   Matches: 416
Best Local Similarity: 94.12%   Conservative: 3
Query Match: 91.69%   Mismatches: 7
DB: 4   Indels: 16
                                         Gaps: 1

US-09-670-568C-1 (1-448) x US-09-542-615A-335 (1-4849)

Qy   1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db   145 ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGCCCAGAGGTTTCCAGCATATCTGG 204

Qy   21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db   205 GATTTTCTGGAACAGCCTATATGTTCAGTTCAGCCCATTGACTTGAACTTTGTGGATGAA 264

Qy   41 ProSerGluAspGlyAlaThrAsnLysIleSerMetAspCysIleArgMetGln 60
Db   265 CCATCAGAAGATGGTGCGACAAACAAGATTAGCATGGACTGCATTCGCATGCAG 324

Qy   61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db   325 GACTCGGACCTGAGTGACCCCATGTGGCCCCAGTACACGAACCTGGGGCTCCTGAACAGC 384

Qy   81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100

Db   385 ATGGACCAGCAGATTCAGAGACGGCTCCTCGTCCACCAGTCCCTATAACAGACCACGCG 444

Qy   101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerThrAspAlaLeu 120
Db   445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCAGCTCCACCTTCGATGCTCTC 504

Qy   121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyHisSerPheAspVal 140
Db   505 TCTCCATCACCCGCCATCCCTTCCAACACCGACTACCCAGGCCCGACAGTTTCGACGTG 564

Qy   141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db   565 TCCTTCCAGCAGTCGAGCACGGCCAAGTCGGCGACTATCGCCACTGGACTGAACTGAAG 624

Qy   161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLeuValMetThrProPro 180
Db   625 AAACTCTACTGCCAAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACCT 684

Qy   181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysAlaGluHisValThrGlu 200
Db   685 CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACCGAG 744

Qy   201 ValValLysArgCysProAsnHisGluSerArgGluAsnGluGlyGlnIleIleAla 220
Db   745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC 804

Qy   221 ProProSerHisLeuIleArgValGluValGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db   805 CCTCCTAGTCATTTGATTCGAGTAGAGGGAACAGCCATGCCCAGTATGTAGAAGATCCC 864

Qy   241 IleThrThrGlyArgGlnSerValLeuValProTyrGlnProProGlnValGlyThrGluPhe 260
Db   865 ATCACAGAGGAACAGAGTGTGCTGGTACCTTATGAGCCACCCCAGGTTGGCACTGAATTC 924

Qy   261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg 280
Db   925 ACGACAGTCTTGTACAATTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT 984

Qy   281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyValLeuLeuGlyArgArgCys 300
Db   985 CCAATTTTAATCATTGTTACTCTGGAAACCAGAGATGGGCAAGTCCTGGGCCGACGCTGC 1044

Qy   301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTGCTTGCCCTGGCCGAGATCGCCGATGAAGAAGATAGCATC 1104

Qy   321 ArgLysGlnGlnValSerAspSerThrLysLysAsnGlyAspThrLysProPheArg 340
Db 1105 AGAAAGCAGCAGGTTTCGGACAGTACCAAGAAGAACGGTGATGGTACGAAGCCCGTTTCGT 1164

Qy   341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCAGATGATGAA 1224

Qy   361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGlnMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATACTTACCAGTGAGGGCCCTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1284

Qy   381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344

Qy   401 GlnGlnGlnHisGlnHisLeuLeuLeuGlnLysHisLeuLeuSerLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCACCAGCACTTACTTCAGAA------ 1374

Qy   421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1375 ----------CAGACCTCAATACAGTCTCCATCTTCATATGGTAACAGCTCC 1416

Qy   441 ProPro 442
Db 1417 CCACCT 1422

us-09-670-568c-1.rni